



FIGURE 7K

	SEQ ID NO:	Genotype
155-160	I/1a	MSTNPQDQRKTKRNTnRPQdvKFPGGGVIGGVYLLPRRGPRIGVRATKKTSERSQPRGRRQPICKarpegrswaqpgvPMPlygnEGGcgWAGH
161-176	II/1b	---N---K-K---NR-Q-V-----L---AT---T-----KA-RPE-RT-AQ--Y---L-GN-CG----
177-180	III/2a	---N---K-K---NR-Q-V-----L---AT---T-----KA-RPE-Ra-AQ--Y---L-gn-mG----
181-185	IV/2b	---N---K-k---NR-Q-v-----L---at---t-----KD-RSt-KS-GK-Y---L-GN-LG----
186	2c	---N---K-K---NR-Q-V-----L---at---t-----KD-RSt-Ks-GK-Y---L-GN-CG----
187-190	(V)/3a	---N---K-K---NR-Q-V-----L---AT---T-----KD-Rtt-KS-GR-Y---L-GN-LG----
191	4a	---L---K-K---IR-Q-y-----V---AT---T-----KA-RSE-RS-AQ--Y---L-GN-CG----
193	4b	---N---K-K---NR-M-V-----L---AT---T-----KA-QPE-RS-AQ--Y---L-GN-CG----
195	4c	---N---K-K---NR-M-V-----L---AA---T-----KA-RSE-RS-AQ--Y---L-GN-CG----
197	4d	---N---K-K---NR-M-V-----L---at---t-----KA-RSE-RS-AQ--Y---L-GN-CG----
199	4e	---N---K-K---NR-M-V-----L---AT---T-----KA-qLE-RS-AQ--Y---L-GN-CG----
192	4f	---N---K-K---NR-M-V-----L---AT---T-----QA-RSE-RS-AQ--Y---L-GN-CG----
198-205	5a	---N---K-K---NR-Q-V-----L---AT---T-----KA-RSE-RS-AQ--Y---L-GN-CG----
206	6a	---L---K-K---NR-T-V-----L---AT---T-----KA-Qpt-RS-GQ--Y---L-AN-Lg----
		---L---K-K---NR-T-V-----L---AT---T-----KA-QPQ-RH-AQ--Y---L-GN-CG----

SEQ ID NO:	Genotype	100	110	120	130	140	150	160	170	180	190	
		LLSPGSRPSWgptPRrrSRNlGKVDTlTGcfADLNGYiPlVGaPlGGvArALANGVRVlEDGvNYATGNlPGCSFSIFlLALlSClTvPaSa										
155-160	I/1a	---	R-R-S-PT---	RR---	L-K---	L-GF---	l-l-A-L-A-R---	VL---	V-Y---	L-S---	L-LTV-ASA	
161-176	II/1b	---	R-s-Pt---	RR---	L-K---	L-GF---	l-l-a-l-a-R---	VL---	V-Y---	L-S---	L-LTi-aSa	
177-180	III/2a	---	R-R-S-Pn---	HR---	V-K---	L-gf---	i-V-a-l-V-R---	VL---	V-Y---	L-S---	L-LTi-vSa	
181-185	IV/2b	---	R-r-t-PT---	HR---	L-k---	L-GF---	l-V-A-V-V-R---	VL---	l-Y---	L-S---	L-LfTV-VSA	
186	2c	---	R-R-S-PT---	HK---	L-K---	L-GF---	l-V-A-V-V-R---	VL---	l-Y---	L-S---	L-LSV-VSA	
187-190	(V)/3a	---	R-R-S-PN---	RR---	L-K---	L-GF---	l-l-A-V-V-R---	AL---	l-F---	L-S---	L-LfLiH-AAS	
191	4a	---	R-R-S-PN---	RR---	L-K---	L-GF---	l-l-A-V-V-R---	AV---	l-Y---	L-S---	L-LTV-ASA	
193	4b	---	R-R-S-PN---	RR---	L-K---	L-GF---	l-l-A-V-V-R---	AV---	l-Y---	L-S---	L-LTT-ASA	
195	4c	---	R-R-S-PN---	RR---	L-K---	L-GF---	l-l-A-V-V-R---	AV---	l-Y---	L-S---	L-LTV-tSA	
197	4d	---	R-R-S-PN---	RR---	L-K---	L-GF---	l-V-A-V-V-R---	LL---	V-Y---	L-S---	L-LTV-ASA	
194	4e	---	R-R-S-QN---	RR---	L-K---	L-GF---	l-l-A-V-V-R---	AL---	l-Y---	L-S---	L-LTT-ASA	
192	4f	---	R-R-S-PN---	RR---	L-K---	L-GF---	l-l-A-V-V-R---	AV---	l-Y---	L-S---	L-LTV-ASA	
198-205	5a	---	R-R-n-PN---	Rk---	L-K---	L-GF---	l-l-G-V-V-R---	VL---	V-Y---	L-S---	L-Ltv-aSa	
206	6a	---	R-R-H-PN---	RR---	L-K---	L-GF---	l-V-A-l-V-A---	Al---	l-Y---	L-S---	L-LTT-ASA	

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

Bukh et al.

Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET



C GENE

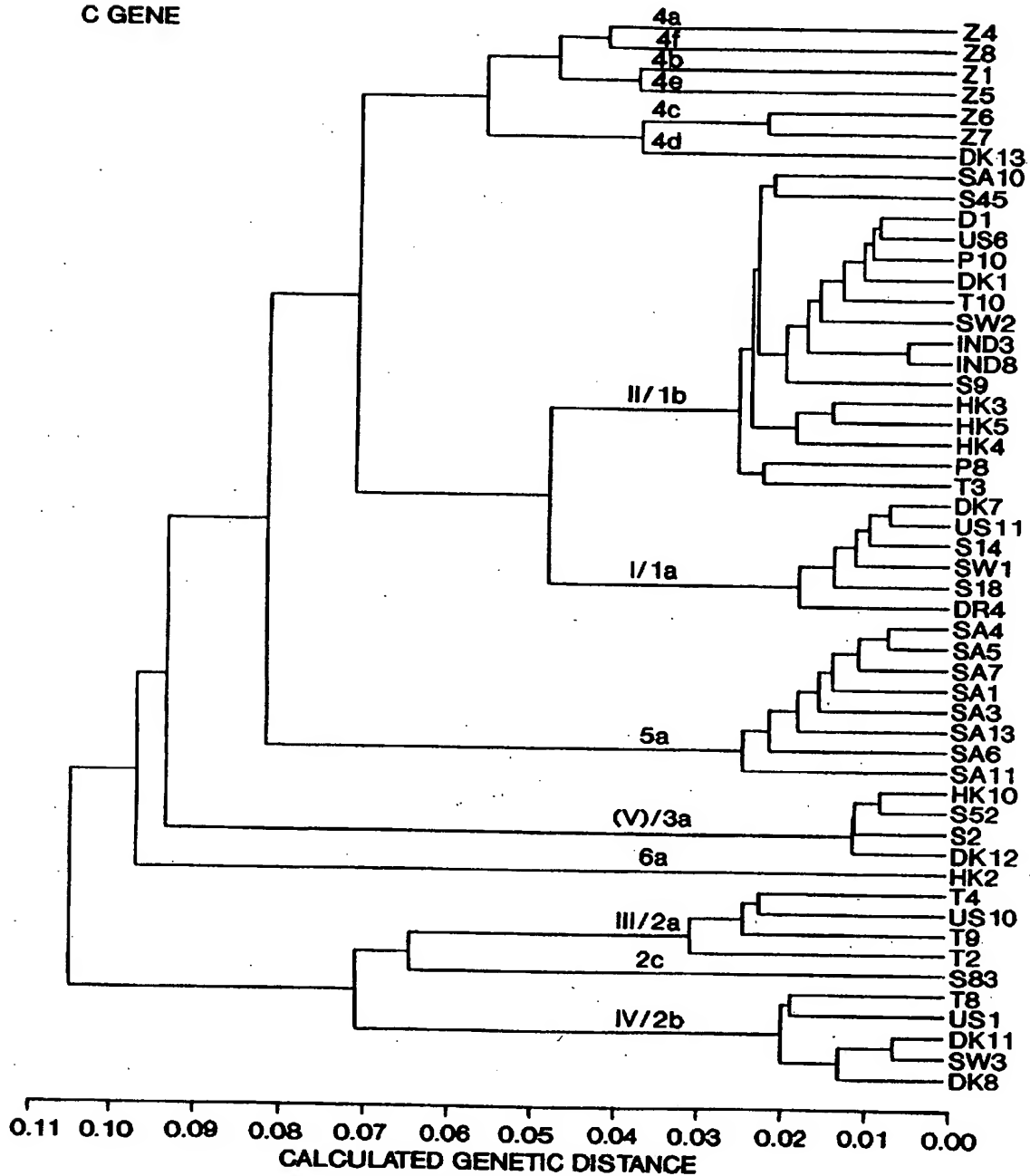


FIG. 8A

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

Bukh et al.

Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

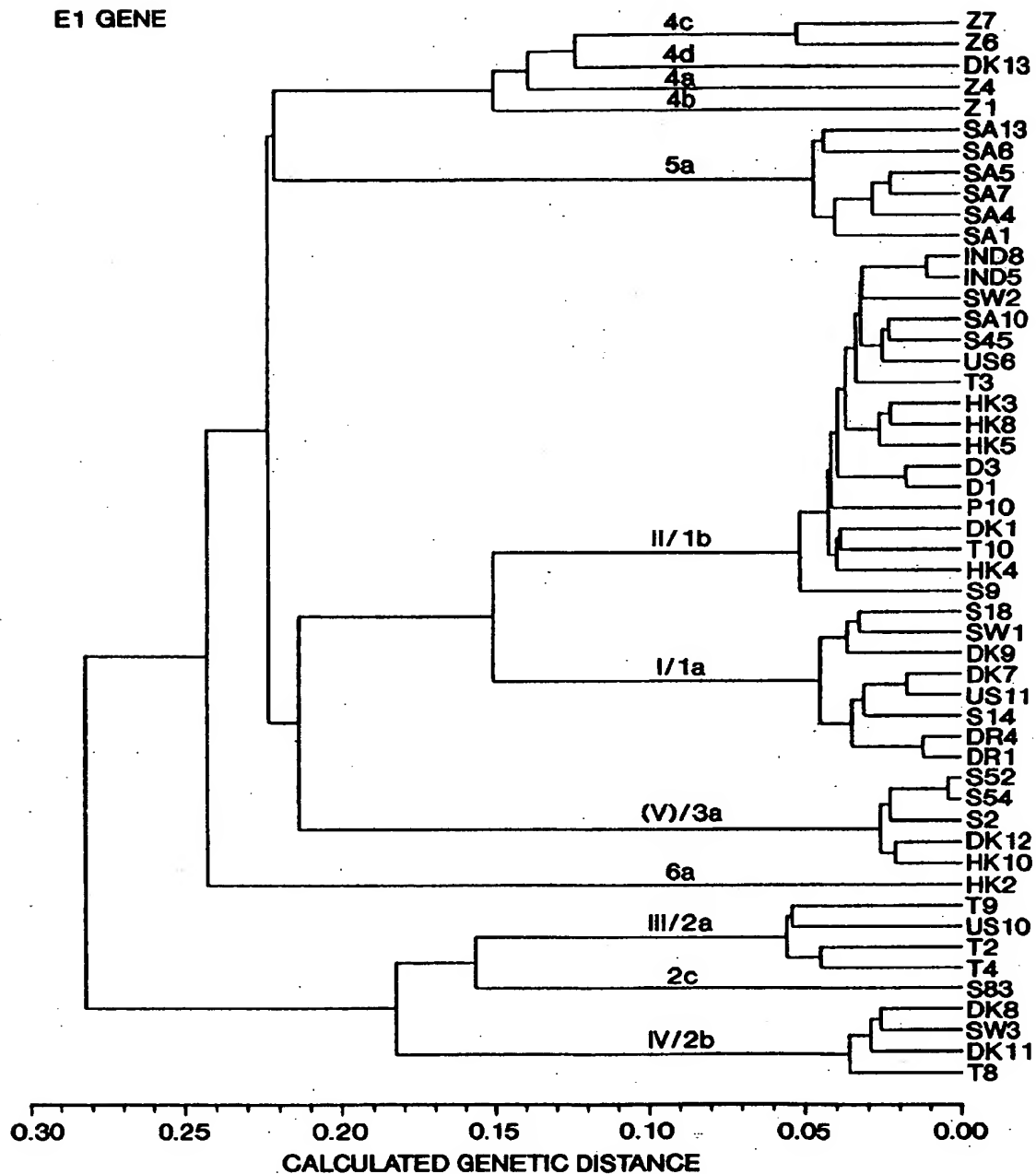


FIG. 8B

SEQ ID NO:	Isolate	1-8
5	S14	1 TACCAAGTGCAGAACTCCACGGGGCTTTACCAATGTTACCAATGATTTGCCCTAACTCGAGTA 1 TACCAAGTGCAGAACTCCACGGGGCTTTACCAATGTCACCAATGATTTGCCCTAACTCGAGTA 8 TACCAAGTGCAGAACTCCACGGGGCTTTACCAATGTCACCAATGATTTGCCCTAACTCGAGTA 4 TACCAAGTGCAGAACTCCACGGGGCTTTACCAATGTCACCAATGATTTGCCCTAACTCGAGTA 3 TACCAAGTGCAGAACTCCACGGGGCTTTACCAATGTCACCAATGATTTGCCCTAACTCGAGTA 2 TACCAAGTGCAGAACTCCACGGGGCTTTACCAATGTCACCAATGATTTGCCCTAACTCGAGTA 6 TACCAAGTGCAGAACTCCACGGGGCTTTACCAATGTCACCAATGATTTGCCCTAACTCGAGTA 7 TACCAAGTGCAGAACTCCACGGGGCTTTACCAATGTCACCAATGATTTGCCCTAACTCGAGTA 1-8 consensus tACCAAGT-CGCAACTCcaCgGGGCTtTACCAATGTCACCAATGATTTGCCCTAACTCGAGTA
5	S14	62 TtGTGTACGAGaCaGctGATGctATCCTaCAGcTCCGGGaTGTGTCCCTTGCGTTcGTGA 1 TcGTGTACGAGGCGGCCGATGCCATCCTGCACACTCCGGGGTGTGCCCTTGCGTTcGCGA 8 TtGTGTACGAGGCGGCCGATGCCATCCTGCACACTCCGGGGTGTGTcCTTGCGTTcGCGA 4 TtGTGTACGAGGCGGCCGATGCCATCCTGCACACGCGGGGTGTGTCCCTTGCGTTcGCGA 3 TtGTGTACGAGGCGGCCGATGCCATCCTGCACGCGGGGTGTGTCCCTTGCGTTcGCGA 2 TtGTGTACGAGGCGGCCGATGCCATCCTGCATCTCCaGGGTGTGTCCCTTGCGTTcGCGA 6 TtGTGTACGAGGCGGCCGATGCCATCCTGCATCTCCgGGGTGTGTCCCTTGCGTTcGCGA 7 TtGTGTACGAGGCGGCCGATGCCATCTACACTCTCCaGGGTGTGTCCCTTGCGTTcGCGA 1-8 consensus TtGTGTACGAGGcGgCcGATgCcATcCTgCac-cCtCCgGgGTGTGTcCTTGCGTTcGCGA

FIGURE 1A-2

SEQ ID NO:	Isolate	
5	S14	123 GGGTAACacCTCGAGGTGTTGGGTGGCGATGACCCCAACGGTGGCCACCAGGGACGGCAAA
1	DK7	123 GGGTAACGtCTCGAGGTGTTGGGTGGCGATGACCCCAACGGTGGCCACCAGGGATGGCAAA
8	US11	123 GGGTAACGCTTCGAGGTGTTGGGTGGCGATGACCCCAACGGTGGCCACCAGGGACGGCAAA
4	DR4	123 GGGTAACaCTCGAGGTGTTGGGTGGCGGTGACCCCAACGGTGGCCACCAGGGACGGCAAA
3	DR1	123 GGGTAACGCTTCGAGGTGTTGGGTGGCGGTGACCCCAACGGTGGCCACCAGGGACGGCAAA
2	DK9	123 GGGTAACGCTTCGAAATGTTGGGTGGCGGTGACCCCAACGGTGGCCACCAGGGACGGCAAG
6	S18	123 GGGTAACGCTTCGAGATGTTGGGTGGCGGTGACCCCAACGGTGGCCACCAGGGACGGCAAA
7	SW1	23 GGAaggCGCCcCGAagTGTGGGTGGCGGTGGCGGTGACCCCAACGGTGGCCACCAGGGACGGCAAA
1-8	consensus	GGGTaaGgcctCGAggTGTGGGTGGCGGTGgaCCCCCAACgGTgGCCACcAGGGACGGCAAA
SEQ ID NO:	Isolate	
5	S14	184 CTCCCCgCaaCGCAGCTTCGACGTtACATCGATCTGCTtGTCTGGGAGcGCCACCCCTCTGTT
1	DK7	184 CTCCCCACagCGCAGCTTCGACGTtCACATCGATCTGCTtGTCTGGGAGtGCCACCCCTCTGTT
8	US11	184 CTCCCCAaACGCAaCTTCGACGTtCACATCGATCTGCTtGTCTGGGAGCGCCACCCCTCTGTT
4	DR4	184 CTCCCCAaACGCACTcCGACGTtCACATCGACCTGCTtGTCTGGGAGCGCCACCCCTCTGCT
3	DR1	184 CTCCCCAaACGCACTTCGACGTtCACATCGACCTGCTtGTCTGGGAGCGCCACCCCTCTGCT
2	DK9	184 CTCCCCGCAaCGCAGCTTCGACGTtCACATCGATCTGCTtGTCTGGGAGCGCCACCCCTCTGCT
6	S18	184 CTCCCCGCAaCGCAGCTTCGACGTtCACATCGATCTGCTtGTtGGGAGCGCCACCCCTCTGCT
7	SW1	184 CTCCCTtGCAaCGCAGCTTCGACGTtCACATCGATCTGCTtGTtGGaAGCGCCACCCCTCTGCT
1-8	consensus	CTCCCCc-CaaCGCAGCTtCGACGTtCACATCGATCTGCTtGTtGGgAGcGCCACCCCTCTGCT

Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

SEQ. ID NO.	Isolate	
5	S14	CGGCCCTCTACGTGGGGACCTGTGCGGGTCTGTCTTTCTGTGCGGTCACTGTTTACCTT
1	DK7	CGGCCCTCTACGTGGGGACCTGTGCGGGTCTGTCTTTCTGTGCGGTCACTGTTTACCTT
8	S11	CGGCCCTCTACGTGGGGACCTGTGCGGGTCTGTCTTTCTGTGCGGTCACTGTTTACCTT
4	DR4	CGGCCCTCTACGTGGGGACCTGTGCGGGTCTGTCTTTCTGTGCGGTCACTGTTTACCTT
3	DR1	CGGCCCTCTACGTGGGGACCTGTGCGGGTCTGTCTTTCTGTGCGGTCACTGTTTACCTT
2	DK9	CGGCCCTCTATGTGGGGACCTGTGCGGGTCTGTCTTTCTGTGCGGTCACTGTTTACCTT
6	S18	CGGCCCTCTATGTGGGGACCTGTGCGGGTCTGTCTTTCTGTGCGGTCACTGTTTACCTT
7	SW1	CGGCCCTCTACGTGGGGACCTGTGCGGGTCTGTCTTTCTGTGCGGTCACTGTTTACCTT
1-8	consensus	CGGCCCTCTACGTGGGGAC - TGTGCGGGTCTGTCTTTCTGTGCGGTCACTGTTTACCTT
5	S14	CTCTCCAGGCGCCCTCTGGACGACGCAAGACTGCAATTGTTCTATCTATCCCGGCCATATA
1	DK7	CTCTCCAGGCGCCACTGGACGACGCAAGGTGCAATTGTTCTATCTATCCCGGCCATATA
8	S11	CTCTCCAGGCGCCACTGGACGACGCAAGGTGCAATTGTTCTATCTATCCCGGCCATATA
4	DR4	CTCTCCAGGCGCCACTGGACGACGCAAGGTGCAATTGTTCTATCTATCCCGGCCATATA
3	DR1	CTCTCCAGGCGCCACTGGACGACGCAAGGTGCAATTGTTCTATCTATCCCGGCCATATA
2	DK9	tTCTCCAGGCGCCACTGGACGCAAGACTGCAATTGTTCTATCTATCCCGGCCATATA
6	S18	CTCCCCAGGCGCCACTGGACGCAAGACTGCAATTGTTCTATCTATCCCGGCCATATA
7	SW1	CTCCCCAGGCGCCACTGGACGCAAGACTGCAATTGTTCTATCTATCCCGGCCATATA
1-8	consensus	cTctCCCAGGCGCCaCTGGACaACGCAaGACTGTTCTaTCTATCCCGGCCATATA

FIGURE 1A-4

SEQ ID NO:	Isolate	
5	S14	367 ACGGTCATCGCATGGCaTGGGATATGATGAACCTGGTCCCCTACgACGGCaCTGGTAG
1	DK7	367 ACGGTCACCGCATGGCGTGGGATATGATGAACCTGGTCCCCTACcACGCGTTGGTAG
8	S11	367 ACGGTCACCGCATGGCaTGGGATATGATGAACCTGGTCCCCTACgCGCGTTGGTgG
4	DR4	367 ACGGcCACCGCATGGCGTGGGATATGATGAACCTGGTCCCCTACgACAGCGCTGGTAG
3	DR1	367 ACGGgCACCGtATGGCaTGGGATATGATGAACCTGGTCCCCTACgACAGCGCTGGTAA
2	DK9	367 ACGGTCATCGcATGGCGTGGGATATGATGAACCTGGTCCCCTACAGCAGCGCTGGTAA
6	S18	367 ACGGTCACCGtATGGCATGGGATATGATGAACCTGGTCCCCTACAAcGCGgtTGGTAA
7	SW1	367 ACGGTCACCGcATGGCATGGGATATGATGAACCTGGTCCCCTACAAcAGCGgtTGGTAG
1-8	consensus	ACGGtCacCGcATGGCaTGGGATATGATGAACCTGGTCCCCTACgAc-GCgcTGGTag
5	S14	428 TAGCTCAGCTGCTCCGGATCCCaCAAGCCATCTTGGATATGATCGCTGGTGTCTCACTGGGG
1	DK7	428 TAGCTCAGCTGCTCCGGATCCCGCAAGCCATCTTGGACATGATCGCTGGTGTCTCACTGGGG
8	S11	428 TAGCTCAGCTGCTCCGGATCCCaCAAGCCATCTTGGACATGATCGCTGGTGTCTCACTGGGG
4	DR4	428 TAGCTCAGCTGCTCCGGATCCCaCAAGCCATCTTGGACATGATCGCTGGTGTCTCACTGGGG
3	DR1	428 TGGCTCAGCTGCTCCGGATCCCaCAAGCCATCTTGGACATGATCGCTGGTGTCTCACTGGGG
2	DK9	428 TGGCGCAGCTGCTCAGGATCCCGCAGGCCATCTTGGACATGATCGCTGGTGTCTCACTGGGG
6	S18	428 TAGCTCAGCTGCTCAGGgTCCCGCAAGCCGCTTGGACATGATCGCTGGTGTCTCACTGGGG
7	SW1	428 TAGCTCAGCTGCTCAGGaTCCCGCAAGCCGCTTGGACATGATCGCTGGTGTCTCACTGGGG
1-8	consensus	TagCTCAGCTGCTCCGGATCCC-CAAGCCaTCTTGGAcATGATCGCTGGTGTCCcCACTGGGG

FIGURE 1A-5

SEQ ID NO:	Isolate	
5	S14	489 AGTCCTAGCGGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTaGTgGTG
1	DK7	489 AGTCCTgCGGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTGGTAGTG
8	S11	489 AGTCCTAGCGGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTGGTAGTG
4	DR4	489 AGTCCTAGCGGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTGGTAGTG
3	DR1	489 AGTCCTAGCGGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTGGTAGTG
2	DK9	489 AGTCCTAGCGGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTGGTAGTG
6	S18	489 AGTCCTAGCGGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTGGTAGTG
7	SW1	489 AGTCCTAGCGGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTGGTAGTG
1-8	consensus	AGTCCTAGCGGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTGGTAGTG

SEQ ID NO:	Isolate	
5	S14	550 CTGCTGCTATTcGCCGGCGTtGACGCG
1	DK7	550 CTGCTGCTATTtGCCGGCGTcGACGCG
8	US11	550 CTGCTGCTATTtGCCGGCGTcGACGCG
4	DR4	550 CTGTTGCTGTTtGCCGGCGTtGATGCG
3	DR1	550 CTGTTGCTGTTtGCCGGCGTtGATGCG
2	DK9	550 CTGTTGCTGTTaCCGGCGTcGATGCG
6	S18	550 CTGTTGCTGTTtCCGGCGTcGATGCG
7	SW1	550 CTGTTGCTGTTtCCGGCGTcGATGCG
1-8	consensus	CTGtTGCTgTtTtgcCGGCGGTcGAtGGCG

FIGURE 1B-1

SEQ ID NO:	Isolate	
11	DK1	1 TATGAAGTGGCAACGCTGTCCGGGGTGTACCAcGTCAaAACGACTGCTCCAACtCAAGCA
24	T10	1 TATGAAGTGGCAACGCTGTCCGGGaTGtACCAcGTCAcGaAACGACTGCTCCAACtCAAGCA
10	D3	1 TATGAAGTGGCAACGCTGTCCGGGGTGTACCAaGTCAcAaATGACTGTtCCAACtCGAGCA
9	D1	1 TATGAAGTGGCAACGCTGTCCGGGGTGTACCAcGTCAcGAaCGACTGTtCCAACtCGAGCA
14	HK5	1 TATGAAGTGGCAACGCTGTCCGGGGTATACCAcGTCAcGAaCGACTGCTCCAACtAAGCA
15	HK8	1 TATGAAGTGGCAACGCTGTCCGGGATATACCAcGTCAcGAaCGACTGCTCCAACtCAAGCA
12	HK3	1 TATGAAGTGGCAACGCTGTCCGGGATATACCAcGTCAcGAaCGACTGCTCCAACtCAAGGg
23	T3	1 TAcGAAGTGGCAACGCTGTCCGGGGTGTACTATGTCAcGAaCGACTGTtCCAACtCAAGCA
22	SW2	1 TATGAAGTGGCAACGCTGTCCGGGGTGTATCATGTCAcGAaCGACTGTtCCAACtCAAGCA
17	IND8	1 TATGAGTGGCAACGCTGTCCGGGGTGTACCAcGTCAcGAaCGACTGCTCCAACtCAAGTA
16	IND5	1 TATGAAGTGGCAACGCTGTCCGGGGTGTACCAcGTCAcGAaCGACTGCTCCAACtCAAGTA
21	SA10	1 TATGAAGTGGCAACGCTGTCCGGGaTGtACCAcGTCAcGAaCGACTGCTCCAACtCAAGCA
20	S45	1 TATGAAGTGGCAACGCTGTCCGGGGcGTACCAcGTCAcGAaCGACTGCTCCAACtCAAGCA
25	US6	1 TATGAAGTGGCAACGCTGTCCGGGATGTACCAcGTCAcGAaCGACTGCTCCAACtCAAGCA
13	HK4	1 cATGAAGTGCaCAACGTATCCGGGATcTACCAcGTCAcGAaCGACTGCTCCAACtCAAGTA
18	P10	1 TATGAAGTGGCAACGCTGTCCGGGGTGTACCAcGTCAcGAaCGACTGCTCCAACtCAAGTA
19	S9	1 TATGAAGTGGCAACGTATCCGGGGcGTACCAcGTCAcGAaCGACTGCTCCAACtCAAGTA
9-25	consensus	tAtGAaGTGcgCAACGTgTCCGGGGgtgTaccAtGTCAcGAaCGACTGcTCCAACtcaAGca

FIGURE 1B-2

SEQ ID NO:	Isolate	
11	DK1	62 TcGTGTATGAGGCAGtGGACgTGATCATGcATACCCCaGGGTGCGTGCCTGCCTTCGGGA
24	T10	62 TtGTGTtTGAGGCAGCGGACtTGATCATGCACACCCCGGGTGCCTGCCTTCGGGA
10	D3	62 TcGTGTATGAGACAGCGGACATGATCATGCACACCCCGGGTGCCTGCCTTCGGGA
9	D1	62 TtGTGTATGAGACAGCGGACATGATCATGCACACCCCGGGTGCCTGCCTTCGGGA
14	HK5	62 TCGTGTACGAGACaACCGGACATGATCATGCACACCCCGGGTGCCTGCCTTCGGGA
15	HK8	62 TCGTGTATGAAACAGCGGACATGATtATGCATACCCCTGGATGCCTGCCTTCGGGA
12	HK3	62 TCGTGTATGAGACAGCaGACATGATCATGCATACCCCTGGATGCCTGCCTTCGGGA
23	T3	62 TTGTGTATGAGACAGCGGACATGATCATGCACACCCCTGGTGCCTGCCTTCGGGA
22	SW2	62 TTGTGTATGAGACAGCGGACATGATCATGCATACCCCGGGTGCCTGCCTTCGGGA
17	IND8	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCGGGTGCCTGCCTTCGGGA
16	IND5	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACTCCCGGGTGCCTGCCTTCGGGA
21	SA10	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCGGGTGCCTGCCTTCGGGA
20	S45	62 TTGTGTATGAGGCAGtGGACgTGATCctTGACACACCCCTGGTGCCTGCCTTCGGGA
25	US6	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACTCCCGGGTGCCTGCCTTCGGGA
13	HK4	62 TTGTGTATGAGGCAGCGGACATGATCATGCATACCCCGGGTGCCTGCCTTCGGGA
18	P10	62 TTGTGTATGAGGCAGCGGACATGATaATGCACACCCCGGGTGCCTGCCTTCGGGA
19	S9	62 TTGTGTACGAGGCAGCGGACgTGATcATGCATACCCCGGGTGTGTaCCCTGCCTTCaGGGA
9-25	consensus	TtGTGTatGAggCagcgGACaTGATcaTGcACACCCCGGGgTGcgTgCCCTGcGtTcGgGA

FIGURE 1B-3

SEQ ID NO:	Isolate	
11	DK1	123 GaaCAACcaCTCCCGtTGCTGGGTAGCGCTCAcCCcACGCTCGCGGCCAGGAACgCCAGC
24	T10	123 GgCAACTCCTCCCGTGTGGGTAGCGTCACTCCcACGCTCGCGGCCAGGAACcACCAGC
10	D3	123 GGACAACTCCTCTCGCTGTGGGTAGCGCTCAcCCcACGCTCGCGGCCAGGAATAGCAGC
9	D1	123 GGACAACTCCTCTCGCTGTGGGTAGCGCTCAcCCcACGCTCGCGGCCAGGAATGGCAaC
14	HK5	123 aAACAACTCCTCCCGTGTGGGTAGCGCTGcCCCCACGCTCGCGGCCAGGAACgCCAGC
15	HK8	123 GAACAACTCCTCCCGTGTGGGTGCGGTCACTCCcACGCTCGCGGCCAGGAATGTcAGC
12	HK3	123 GAACAACTCCTCCCGTGTGGGTAGCGCTCACTCCcACGCTCGCGGCCAGGAACGTcAGC
23	T3	123 GAgCAATTCCTCCCGTGTGGGTAGCGCTtACTCCcACGCTCGCGGCCAGGAACGCCAGC
22	SW2	123 GGcCAACTCCTCCCGTGTGGGTAGCGCTCACTCCcACGCTAGCaGCCAGGAACaCCAGC
17	IND8	123 GGGCAACTtCTCTAgTtTGCTGGGTAGCGCTCACTCCcACTCTCGCGGCCAGGAACGCCAGC
16	IND5	123 GGGCAACTCCTCTCGCTGTGGGTAGCGCTCACTCCcACTCTCGCGGCCAGGAACGCCAGC
21	SA10	123 GAACAACTCCTCCCGTGTGGGTAGCGCTCACTCCcACGCTCGCGGCCAGGAACCTCCAGC
20	S45	123 GAACAACTCCTCCCGtTGCTGGGTGCGGTCACTCCcACGCTCGCGGCCAGGAACCTCCAGC
25	US6	123 GAACAACTCCTCCCGTGTGGGTAGCGCTCACTCCcACGCTCGCGGCCAGGAACGTtAGC
13	HK4	123 GAACAACTCCTCCCGtTGCTGGGTAGCGCTCACTCCcACGCTCGCGGCCAGGAACGCCAGC
18	P10	123 GAACAACTCCTCCCGTGTGGGTAGCGCTCACTCCcACaCTCGCGGCCAGGAATtCCAGC
19	S9	123 GggtAACTCTCCCAaTGCTGGGTgGCGCTCAcCCcCAcGCTCGCGGCCAGGAACgCtAcC
9-25	consensus	gaacAActcCTCccgctGcTGGGGTaGCGCTcaCtCCCACgCTcGCGGCCAGGAACgcccAgC

FIGURE 1B-4

SEQ. ID NO:	Isolate	
11	DK1	184 aTCCCCACTACGACaATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
24	T10	184 GTCCCCACTACGACgATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
10	D3	184 GTCCCCACTACGACaATACGACGCCACGTGCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
9	D1	184 GTCCCCACTACGGGgATACGACGCCACGTGCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
14	HK5	184 GTCCCCACaACGGCAATACGACGCCACGTGCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
15	HK8	184 GTCCCCACTACGACaATACGACGCCACGTGCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
12	HK3	184 GTCCCCACcACGACAATACGACGTCACTGCGATTGCTCGTTGGGGCGGCTGCCTTCTGCT
23	T3	184 GTCCCCACTAaGACAATACGACGTCACTGCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
22	SW2	184 GTCCCCACTACGACaATACGACGCCACGTGCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
17	IND8	184 GTCCCCACcACGACAATACGACGCCACGTGCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
16	IND5	184 GTcTCCACcACGACAATACGACaCCACGTGCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
21	SA10	184 GTCCCCACTACGACaATACGACGCCACGTGCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
20	S45	184 GTCCCCACTACGACAATACGACGTCACTGCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
25	US6	184 GTCCCCACTACGACAATACGACGCCACGTGCGATTGCTCGTTGGGGCGGCTaCTTTCTGCT
13	HK4	184 aTCCCCACTACGACAATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
18	P10	184 GTCCCCACTACGgCAATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
19	S9	184 GTCCCCcACcACGaCAATACGACGTCAITGCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
9-25	consensus	gTCCcCcAcTAcGaCaATACGACgCaCGTCGATTTTGCTCGTTGGGGCGGCTgctTTCTGCT

FIGURE 1B-5

SEQ ID NO:	Isolate	
11	DK1	245 CCGCTATGTACGTGGGGACCTCTGCGGATCgTTTTCTCGTCTCTCAGCTGTTACCTTT
24	T10	245 CCGCTATGTATGTGGGaGACCTCTGCGGATCTGTTTTCTCGTCTCTCAGCTGTTACCTTT
10	D3	245 CCGCCATGTACGTGGGGATCTcTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTTT
9	D1	245 CCGCCATGTACGTGGGGATCTcTGCGGATCTGTTTTCTCTCaTCTCCAGCTGTTACCCcT
14	HK5	245 CCGCTATGTACGTGGGGATCTcTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTTT
15	HK8	245 CCGCTATGTACGTGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTTT
12	HK3	245 CCGCTATGTACGTGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTTT
23	T3	245 CCGCTATGTACGTGGGGATCTcTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTTT
22	SW2	245 CCGtTATGTACGTGGGGATCTcTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTTT
17	IND8	245 CCGCTATGTACGTGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTTT
16	IND5	245 CCGCTATGTACGTGGGGATCTaTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTTT
21	SA10	245 CCGCcATGTACGTGGGGAcCTCTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTTT
20	S45	245 CCGCTATGTACGTGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTTT
25	US6	245 CCGCTATGTACGTGGGGAcCTCTGCGGGTCCGTTTTCTCTCaTCTCCAGCTGTTACCTTT
13	HK4	245 CCGCcATGTACGTGGGaGATCTCTGCGGATCTGTcTTCTCGTCTCCAGTGTGTTACCTTT
18	P10	245 CCGCTATGTACGTGGGGATCTCTGCGGATCTGTTcTCTCGTCTCCAGCTGTTACCTTT
19	S9	245 CCGCTATGTACGTGGGGAcCTgTGCGGATCTGTTtTCTCTCaTCTCCAGCTGTTACCCaT
9-25	consensus	CCGctATGTACGTGGGgGATCTcTGCGGATCtGTtTtTCTCTcgTcTcCcCAGcTGTTCACcctT

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FIGURE 1B-6

SEQ ID NO:	Isolate	
11	DK1	306 tTCaCTCGCCGGCATGAGACagcaCAGGACTGCAACTGCTCAATCTATCCCGGCCAcgTt
24	T10	306 CTGCGCTCGCCGGCATGAGACTtTgCAGGACTGCAACTGCTCAATCTATCCCGGCCAcTtG
10	D3	306 CTGCGCTCGCCGGCATGAGACaGTACAGGAaTGTAACTGCTCAATCTATCCCGGCCAcGtG
9	D1	306 CTGCGCTCGCCGGCATGAGACGGTACAGGAGTGTAACTGCTCAATCTATCCCGGCCAcGtG
14	HK5	306 CTGCGCTCGCCGGCACACGAGACGGTACAGGACTGCAACTGCTCAATCTATCCCGGCCAcGTA
15	HK8	306 tTCGCTCGCCGGCACACGAGACGGTACAGGACTGCAACTGCTCAATCTATCCCGGCCAcGTA
12	HK3	306 CTGCGCTCGCCGGCACACGAGACAGTACAGGACTGCAACTGCTCACTCTATCCCGGCCAcGTA
23	T3	306 CTGCGCTCGCCGGCAtGAGACAGTACAGGACTGCAACTGCTCAATCTATCCCGGCCAcGTA
22	SW2	306 tTCACCTCGCCGGCACAGACAGTACAGGACTGCAACTGCTCACTCTATCCCGGCCAcGTA
17	IND8	306 CTCACCGCGCCGGCATGAGACAGTACAGGACTGCAATTGCTCCATCTATCCCGGCCAcGTA
16	IND5	306 CTCACCGCGCCGGCATGAGACAGTACAGGACTGCAATTGCTCCATCTATCCCGGCCAcGTA
21	SA10	306 CTGCGCTCGCCGGTAtGAGACAGTACAGGACTGCAATTGCTCAATCTATCCCGGCCGcGTA
20	S45	306 CTGCGCTCGTCGGCATGAGACAGTACAGGACTGCAACTGTTCAATCTATCCCGGCCAcGTA
25	US6	306 CTGCGCTCGTCaGCATGAGACAGTACAGGACTGCAATTGTTCAATCTATCCCGGCCAcGTA
13	HK4	306 CTGCGCTCGCCGGCATGAGAcGTACAGGACTGCAATTGCTCAATCTATCCCGGCCAcGTA
18	P10	306 CTCaCTCGCCGGCATtGACAGTACAGGACTGCAATTGTTCAATCTATCTCTtGGCCAcGTA
19	S9	306 CTCGcCcCGtCGGCATgaGACAGTACAGaACTGCAATTGCTCAATCTATCTCTCCgGacACGTg
9-25	consensus	cTCgCCTCGcCggcAtgaGACagtaCAGgAcTGcAAcTGcTcAaTCTATCTCCcGGcCacgTa

FIGURE 1B-7

SEQ ID NO:	Isolate	
11	DK1	367 TCAGGTCACCGCATGGCTTGGGATATGATGAACTGGTCACTTACAAACAGCCCTAGTGG
24	T10	367 TCAGGTCACCGCATGGCTTGGGACATGATGAACCTGGTCCTACAAACAGCCTTAGTGG
10	D3	367 ACAGGTCACCGCATGGCTTGGGATATGATGAACTGGTCCTACAGCAGCCCTAGTGG
9	D1	367 ACAGGTCACCGCATGGCTTGGGATATGATGAACCTGGTCCTACAAACAGCCTTAGTGG
14	HK5	367 ACAGGTCACCGCATGGCTTGGGATATGATGAACCTGGTCCTACAAACAGCCCTAGTGG
15	HK8	367 TCAGGTCACCGCATGGCTTGGGATATGATGAACTGGTCGCCCAACAGCCCTAGTGG
12	HK3	367 TCAGGTCACCGCATGGCTTGGGATATGATGAACCTGGTCCTACAGCAGCCCTAGTGG
23	T3	367 aCAGGTCACCGtATGGCTTGGGATATGATGAACTGGTCGCCCAaCgGCaCTAGTGG
22	SW2	367 TCAGGTCACCGCATGGCTTGGGACATGATGAACCTGGTCACCTACAGCaGCCCTgGTGG
17	IND8	367 TCAGGTCACCGCATGGCTTGGGATATGATGAACTGGTCACCTACAGCgGCCCTAGTGG
16	IND5	367 TCAGGTCACCGCATGGCTTGGGATATGATGAACCTGGTCACCTACAGCAGCCCTAGTGG
21	SA10	367 ACAGGTCACCGCATGGCTTGGGATATGATGAACCTGGTCACCTACaCAGCtCTAGTaG
20	S45	367 ACAGGTCACCGCATGGCTTGGGATATGATGAACCTGGTCCTACAGCAGCctTAGTGG
25	US6	367 TCAGGTCACCGCATGGCTTGGGATATGATGAATGGTCACCTACAGCAGCCCTAGTGG
13	HK4	367 TCAGGTCACCGCATGGCTTGGGATATGATGAACCTGGTCACCTACAGCAGCCCTAGTGG
18	P10	367 TCAGGTCACCGCATGGCTTGGGATATGATGAACCTGGTCGCCCAACAGCAGCCCTAGTGG
19	S9	367 aCAGGTCatCGCATGGCtTGGGATATGATGAACCTGGTCGCCtACaACAGCCCTAGTGG
9-25	consensus	tCAGGTCaCGcATGGCtTGGGATATGATGAACtGGTCAcCtACAGCaGCCcTaGTg

FIGURE 1B-8

SEQ ID NO:	Isolate	
11	DK1	TaTCGCAGTTACTCCGgaATCCCAAGCTGTCTGGACATGGTgGcGGGGCCCCACTGGGG
24	T10	TgTCGCAGTTACTCCGGATCCCAAGCTGTCTGGACATGGTgCaGGGGCCCCACTGGGG
10	D3	TATCGCAGTTACTCCGGATCCCAAGCTGTCTGGACATGGTGGCGGGCCCCACTGGGG
9	D1	TATCGCAGTTACTCCGGATCCCAAGCTGTCTGGACATGGTGGCGGGCCCCACTGGGG
14	HK5	TGTCGCAGTTACTCCGGATCCCGCAAGCTGTCTGGACATGGTgAGCGGGGGCCCCACTGGGG
15	HK8	TGTCGCAGTTACTCCGGATCCCGCAAGCTaTCGTGGACATGGTGGCGGGCCCCACTGGGG
12	HK3	TGTCGCAaTTACTCCGGATCCCGCAAGCTGTCTGGACATGGTGGCGGGCCCCACTGGGG
23	T3	TGTCGCAGTTgCTCCGGATCCCAAGCTGTCTGGACATGGTGGCGGGCCCCACTGGGG
22	SW2	TATCGCAGTTaCTCCGGATCCCAAGCTGTCTGGACATGGTgAGCGGGGGCCCCACTGGGG
17	IND8	TATCGCAGTTGCTCCGGATCCCAAGCTGTCTGGATATGGTGGCGGGGGCCCCACTGGGG
16	IND5	TATCGCAGTTGCTCCGGATCCCAAGCTGTCTGGATATGGTGGCGGGGGCCCCACTGGGG
21	SA10	TATCGCAGTTACTCCGGATCCCAAGCTaTCGTGGACATGGTGGCGGGGGCCCCACTGGGG
20	S45	TATCGCAGTTACTCCGGATCCCAAGCTGTCTGGACATGGTGGCGGGGGCCCCACTGGGG
25	US6	TATCGCAGTTACTCCGGATCCCAAGCTGTCTGGACATGGTGGCGGGGGCCCCACTGGGG
13	HK4	TATCGCAGTTACTCCGacTCCCAAGCTGTCTGGACATGGTGGCGGGGaGCCCACTGGGG
18	P10	TgTCGCAGTTACTCCGGATCCCAAGCTaTCTGGATgTGGTGGCGGGGGCCCCACTGGGG
19	S9	TaTCGCAGTTACTCCGGATCCCAAGCTgTCTGGATaTGGTGGCGGGGGCCCCACTGGGG
9-25	consensus	TaTCGCAGTtTaCTCCGgaTCCCAaCAAGCTgTCGTGGAcCaTGGTgGcGGGGCCCCACTGGGG

FIGURE 1B-9

SEQ ID NO:	Isolate	
11	DK1	489 AGTCCTGGCGGCTcGCCTACTACTCCATGGCGGGAACTGGGCCAAGGTTTAAATTGTG
24	T10	489 AGTCCTGGCGGCTcGCCTACTACTCCATGGCGGGAACTGGGCTAAGGTTTAAATTGTG
10	D3	489 GGTCTGGCGGCTCGCCTACTATTCCATGTGGGAACTGGGCTAAGGTTTGAATTGTG
9	D1	489 GGTCTGGCGGCTCGCCTACTATTCCATGTGGGAACTGGGCTAAGGTTTGAATTGTG
14	HK5	489 GGTCTGGCGGCTCGCCTACTATTCCATGTGGGAACTGGGCTAAGGTTTGAATTGTG
15	HK8	489 AGTCCTAGCGGCTTGCCCTACTATTCCATGTGGGCAACTGGGCTAAGGTTTGAATTGTG
12	HK3	489 AGTCCTAGCGGCTTGCCCTACTATTCCATGTGGGCAACTGGGCTAAGGTTTGAATTGTG
23	T3	489 AGTCCTGGCGGCTTGCCCTACTATTCCATGTGGGAACTGGGCTAAGGTTTGAATTGTG
22	SW2	489 AGTCCTGGCGGCTTGCaTACTATTCCATGTGGGCAACTGGGCTAAGGTTTGAATTGTG
17	IND8	489 AATCCTGGCGGCTTGCCCTACTATTCCATGTAGGAACTGGGCTAAGGTTTGAATTGTG
16	IND5	489 AATCCTGGCGGCTTGCCCTACTATTCCATGTAGGAACTGGGCTAAGGTTTGAATTGTG
21	SA10	489 AGTCCTaGCGGCTTGCCCTACTATTCCATGTGGGAACTGGGCTAAGGTTTGAATTGTc
20	S45	489 AGTCCTGGCGGCTTGCCCTACTATTCCATGTGGGAACTGGGCTAAGGTTCTGAATTGTG
25	US6	489 AGTCCTGGCGGCTTGCCCTACTATTCCATGTGGGAACTGGGCTAAGGTTCTGAATTGTG
13	HK4	489 AGTCCTaGCGGCTTGCTTACTATTCCATGTGGGAACTGGGCAAGGTTTGAATTGTG
18	P10	489 AGTCCTGGCGGCTTGCCCTACTATTCCATGTGGGAACTGGGCTAAGGTTCTGAATTGTG
19	S9	489 AGTCCTGGCGGCTcGCCTACTATTCCATGTGGGAACTGGGCTAAGGTTTGAATTGTG
9-25	consensus	agTCCTgGCGGCTTGCCCTACTATTCcATGGtgGgAACTGGGCTAAGGTTtTgATTGTg

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FIGURE 1B-10

SEQ ID NO:	Isolate	
11	DK1	550 tTGCTACTCTTTGGCCGGCGTTGATGGG
24	T10	550 ATGCTACTCTTTGGCCGGCGTTGATGGG
10	D3	550 ATGCTACTCTTTGCTGGCGTGACGGC
9	D1	550 ATGCTACTCTTTGCTGGCGTTGACGGC
14	HK5	550 ATGCTACTCTTTGGCCGGCGTTGATGGG
15	HK8	550 ATGCTACTCTTTGGCCGGCGTTGATGGG
12	HK3	550 ATGCTACTCTTTGGCCGGCGTTGATGGG
23	T3	550 CTGCTACTCTTTGGCCGGCGTTGATGGG
22	SW2	550 ATGCTACTCTTTGCTGGCGTTGACGGG
17	IND8	550 ATGCTACTCTTTGGCCGGCGTTGACGGG
16	IND5	550 ATGCTACTCTTTGGCCGGCGTTGACGGG
21	SA10	550 ATGCTACTCTTTGGCCGGCGTTGACGGG
20	S45	550 ATGCTACTCTTTGGCCGGCGTTGACGGG
25	US6	550 tTGCTACTCTTTGGCCGGCGTTGACGGG
13	HK4	550 ATGCTACTCTTTGGCCGGCGTTGACGGG
18	P10	550 ATGCTACTCTTTGGCCGGCGTTGACGGa
19	S9	550 ATGCTACTCTTTGCTGGTGTGACGGG
9-25	consensus	aTGCTACTCTTTGGCCGGCGTTGACGGG

FIGURE 1C-1

SEQ ID NO:	Isolate	
26	T2	1 GCCCAAGTGAGGAACACACAGccgCgGtTACATGGTGACTAACGACTGTTCcAATGAGAGCA
27	T4	1 GCaCAAGTGAAGAACACACcAcTaaCAGCTACATGGTGACcAACGACTGTTCtAATGACAGCA
28	T9	1 GCCgAAGTGAAGAAACACcAGTACCAGCTACATGGTGACaAATGACTGTTCcAACGACAGCA
29	US10	1 GtCcAAGTGAAaAAACACcAGTACCAGCTAtATGGTGACcAATGACTGcTCCAACGACAGCA
26-29	consensus	GcccAAGTGAagAACACcAgtaCAGcTAcATGGTGACcAA - GACTGtTCCAA - GAcAGCA
SEQ ID NO:	Isolate	
26	T2	62 TCACcTGGCAGCTCCaAGCCGCGGTtCTCCACGTCCCCGGGTGTaTCCCGTGTGAGAggct
27	T4	62 TCACtTGGCAGCTCCAGGCGCGGTCTCTCCACGTCCCGGGTGTGTCCCGTGGAGAAaAc
28	T9	62 TCACcTGGCAACTCCAGGCGCGGTCTCTCCACGTCCCCGGGTGcGTCCCGTGGAGAGT
29	US10	62 TCACtTGGCAACTtgAGGctGCGGTCTCTCCACGTtCCCCGGGTGTGTCCCGTGGAGAAAGT
26-29	consensus	TCAC - TGGCA - CTccAGcCGCGGTcCTCCACGTcCCCCGGGTGTgTCCCGTGGcGAGA - agt
SEQ ID NO:	Isolate	
26	T2	123 GGGAAATACATCcCGaTGCTGGATACCGGTcaCACCAAAACGTGGCCGTGGCGGAGCCCGGC
27	T4	123 GGGAAATACATCtCGGTGTGGATACCGGTtTCACCAAAACGTGGCCGTGGCGGAGCCCGGC
28	T9	123 tGGAAAcgCgTCgCGGTGTGGATACCGGTCTCgCCAAACGTaGctGTGCAGCGGCCTGGC
29	US10	123 gGGAAAtaCaTctCGGTGTGGATACCGGTCTCaCCAAAtGTgGccGTGCAGCGGCCTGGC
26-29	consensus	gGGAAAtaCaTctCGgTGCTGGATACCGGTctCaCCAAAcGTgGccGTGC - GC - GCC - GGC

SEQ ID NO:	Isolate	
26	T2	184 GctCttACGCAGGGCTTGGGACGCACATcGACATGGTtGTGATGTCCGCCACGCTCTGCT
27	T4	184 GCCCTCAGCAGGGCTTGGGACGCACATtGACATGGTtGTGATGTCCGCCACGCTCTGCT
28	T9	184 GCCCTCAGCAGGGCTTGGGACGCACATCGACATGGTtGTGATGTCCGCCACGCTCTGCT
29	US10	184 GCCCTCAGCAGGGCTTGGGACTcACATCGACATGGTcGTGATGTCCGCCACGCTCTGCT
26-29	consensus	GCcCTcACGCAGGGCTTGGGACgCACATcGACATGGTtGTGATGTCCGCCACGCTCTGCT
26	Isolate	245 CTGCCcCTcTACGTGGGGGACCTCTCGCGGGGGTgATGTCTGCAGCCcAGATGTTcATtGT
27	T4	245 CTGCTCTtTACGTGGGGACCTCTCGCGGGGGTgATGTCTGCAGCCcAGATGTTcATcGT
28	T9	245 CCGCTCTcTACGTGGGGGAtCTCTCGCGGGGGTgATGTCTGCcGcTcCAGATGTTcATtAt
29	US10	245 CCGCTCTtTACGTGGGGGAcTCTCTCGGGtGGGgTgATGTCTGCcAGcCaaATGTTcATtGt
26-29	consensus	C-GCtCT-TACGTGGGGGAccTCTCGGGcGGGgTgATGTCTGCcAGcCAGATGTTcATtGt
26	Isolate	306 CTCGCCGcGcAGcCACTGGTtTGTGCAAGaaTGCAATtGCTCcATCTACCCcGGtACCATC
27	T4	306 CTCGCCGCAACATcACTGGTtTGTGCAAGAcTGCAATtGCTCtATCTACCCtGGcACCATC
28	T9	306 CTCGCCGcAGcACCACTGGTtTGTGcAGGAATGCAACTGCTCCATtTACCCtGGTACCATC
29	US10	306 CTCGCCGcGcCACCACTcGTTTGTGcAGGAATGCAACTGCTCCATcTACCCcGGTACCATC
26-29	consensus	CTCGCCGC - aCacCACTgGTTTGTGCA - GaaTGCAA - TGCTCcATcTACCC - GGtACCATC

FIGURE 1C-3

SEQ ID NO:	Isolate	
26	T2	367 ACTGGACACCGTATGGCATGGGACATGATGATGAACCTGGTCGCCACaGCCACCATGATCC
27	T4	367 ACTGGACACCGTATGGCATGGGATATGATGATGAACCTGGTCGCCACgGCCACCATGATCC
28	T9	367 ACTGGACACCGTATGGCATGGGACATGATGATGAACCTGGTCGCCACaCCACCATGATCt
29	US10	367 ACcGGgCACCGTATGGCATGGGACATGATGATGAACCTGGTCGCCACgCCACTtTGATCC
26-29	consensus	ActGGaCACCGTATGGCATGGGACATGATGATGAACCTGGTCGCCAC-gCCACCaTGATCC
SEQ ID NO:	Isolate	
26	T2	428 TGGCGTACGCGATGCGCGTTCCCGAGGTCAATCaTAGACATCaTcgCGGGGGCtCACTGGGG
27	T4	428 TGGCGTACGCGATGCGCGTTCCCGAGGTCAATcTAGACATCgTLAGCGGGGCaCACTGGGG
28	T9	428 TGGCGTACGCGATGCGCGTTCCCGAGGTCAATCaTAGACATCaTAGCGGaGctCACTGGGG
29	US10	428 TGGCGTACGtGATGCGCGTTCCCGAGGTCAATCaTAGACATCaTtAGCGGgGCGCaCTGGGG
26-29	consensus	TGGCGTACGcGATGCGCGTTCCCGAGGTCAATCaTAGACATCaT-agCGGGgGctCACTGGGG
SEQ ID NO:	Isolate	
26	T2	489 CGTCATGTTtGGCTTGGCCTACTTCTCTATGCAGGAGCGTGGCGGAAGTCaTTGTCAATC
27	T4	489 CGTCATGTTGGCTTGGCCTACTTCTCTATGCAGGAGCGTGGCGGAaGTCGTGTGCATC
28	T9	489 CGTCATGTTGGCCTTAGCCTACTTCTCTATGCAGGAGCGTGGCGGAAGTCGTGTGCATC
29	US10	489 CGTctTGTTGGCctTAGCCTACTTCTCTATGCAGGAGCGTGGCGGAaGTCGTGTGCATC
26-29	consensus	CGTCaTGTTcGGCtT-GCCTACTTCTCTATGCAGGAGCGTGGCGGAa-GTCgTTGTGCATC

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FIGURE 1C-4

SEQ ID NO:	Isolate	
26	T2	550 CTctTGCTGGctGCTGGGGTGGACGCG
27	T4	550 CTtcTGCTGGCCGCTGGGGTGGACGCG
28	T9	550 CTgtTGCTcaCCGCTGGcGTGGACGCG
29	US10	550 CTtcTGCTagCCGCTGGgGTGGACGCG
26-29	consensus	CTt-TGCTggCCGCTGGgGTGGACGCG

FIGURE 1D-1

SEQ ID NO:	Isolate
33	T8
30	DK8
32	SW3
31	DK11
30-33	consensus
62	T8
62	DK8
62	SW3
62	DK11
62	consensus
123	T8
123	DK8
123	SW3
123	DK11
123	consensus
33	T8
30	DK8
32	SW3
31	DK11
30-33	consensus

ATCGCCcGAACgCCACaACTTtACCCa-GAGTGCAACTGTTCcATCTACCAAGGTcAtATC

FIGURE 1D-3

SEQ ID NO:	Isolate	
33	T8	367 ACCGGCCACCGCATGGCATGGGACATGATGCTgAACTGGTCACCAACTCTcACCATGATCC
30	DK8	367 ACCGGCCACCGCATGGCATGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC
32	SW3	367 ACCGGCCACCGCATGGCgTGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC
31	DK11	367 ACCGGCCACCGCATGGCaTGGGACATGATGCTtAACTGGTCACCAACTCTcACCATGATCC
30-33	consensus	ACCGGCCACCGCATGGCaTGGGACATGATGCTaAACTGGTCACCAACTCT - ACCATGATCC
33	T8	428 TCGCCTAcGcTcGTcGTgCCTGAaCTAGtCCTtgAaGTTGTCTTcGGCGGCCcATTGGGG
30	DK8	428 TCGCCTATGCCGCTCGTGTTCCTGAGCTAGccCTTccAgTTGTCTTcGGCGGCCcATTGGGG
32	SW3	428 TcGCCTATGCCGCTCGTGTTCCTGAGCTAGTcCTTGAAGTTGTCTTcGGCGGCCcATTGGGG
31	DK11	428 TcGCCTATGCCGcCcGTGTTCCTGAGCTAGTcCTTGAAGTcGTCTTcGGTGGtCATTTGGGG
30-33	consensus	TcGCCTATGCCGcTcGTGTtCCTGAGCTAGtCCTtgAaGTTGTCTTcGGCGGCCcATTGGGG
33	T8	489 CGTGGTGTtTGGCTTGGCCtATtTCTCCATGCaAGAGCGTGGGCCAAAGTCATcGCCATC
30	DK8	489 CGTGGTGTtTGGCTTGGCCtATtTCTCCATGCaAGAGCGTGGGCCAAAGTCATtGCCATC
32	SW3	489 CGTGGTGTtTGGCTTGGCCtATtTCTCCATGCaAGAGCGTGGGCCAAAGTCATtGCCATC
31	DK11	489 tGTGGTGTtTGGCTTGGCCtATtTCTCCATGCaAGAGCGTGGGCCAAAGTCATtGCCATC
30-33	consensus	CGTGGTGTtTGGCTTGGCCtATtTCTCCATGCa - GGAGCGTGGGCCAA - GTCATtGCCATC

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 1D-4

SEQ ID NO:	Isolate	
33	T8	550 CTCCTcCTTGTcGCAGGAGTGGAcGCA
30	DK8	550 CTCCTtCTTGTcGCAGGAGTGGATGCA
32	SW3	550 CTCCTgCTTGTcGCAGGAGTGGATGCA
31	DK11	550 CTCCTtCTTGTaGCAGGAGTGGATGCA
30-33	consensus	CTCCTtCTTGTcGCAGGAGTGGAtGCA

SEQ ID NO:	Isolate
35	DK12
36	HK10
37	S2
39	S54
38	S52
35-39	consensus
62	DK12
62	HK10
62	S2
62	S54
62	S52
35-39	consensus

1	tTAGAGTGGCGGAATGTGTCCGGCCTCTACGTCTTACCAACGACTGTtCCAATAGCAGTA
1	CTAGAGTGGCGGAATGTGTCTGGCCTCTATGTCTTACCAACGACTGTcCCAATAGCAGTA
1	CTAGAGTGGCGGAATACGTCTGGCCTCTATGTCTcACCAACGACTGTTCCAATAGCAGTA
1	CTAGAGTGGCGGAATACGTCTGGCCTCTATaTCTTACCAACGACTGTTCCAATAGCAGTA
1	CTAGAGTGGCGGAATACGTCTGGCCTCTATgTCTTACCAACGACTGTTCCAATAGCAGTA
	cTAGAGTGGCGGAATacGTCTGGCCTCTAtgTCTTcACCAACGACTGTtCCAATAGCAGTA
62	TcGTGTATGAGGCCGATGACGTcATTCTGCACACACCTGGCTGTGTACCTTGTGTTCAGGA
62	TTGTGTATGAGGCCGATGACGTcATTCTGCACACACCTGGCTGTGTACCTTGTGTTCAGGA
62	TTGTGTATGAGGCCGATGACGTtATTCTGCACACACCTGGCTGTGTACCTTGTGTTCAGGA
62	TTGTGTATGAGGCCGATGACGTcATTCTGCACACACCCGGCTGTGTACCTTGTGTTCAGGA
62	TTGTGTATGAGGCCGATGACGTcATTCTGCACACACCCGGCTGTGTACCTTGTGTTCAGGA
62	TTGTGTATGAGGCCGATGACGTcATTCTGCACACACCCGGCTGTGTACCTTGTGTTCAGGA
35-39	consensus

FIGURE 1E-2

SEQ ID NO:	Isolate	
35	DK12	123 CGGCAATACATcTcAGTGCTGGACCTCaGTGACgCCTACAGTGGCAGTCAGGTACGTcCGGA
36	HK10	123 CGGCAATACATCCACGTGCTGGACCTcGcGTGACaCCTACAGTGGCAGTCAGGTACGTcCGGA
37	S2	123 CGGtAATACATCCACGTGCTGGACCCcAGTGACaCCTACAGTGGCAGTCAGGTATcGTcCGGA
39	S54	123 CGGCAATACATCCACGTGCTGGACCCcAGTGACaCCTACAGTGGCAGTCAGGTACGTcCGGA
38	S52	123 CGGCAATACATCCATcGTGCTGGACCCcAGTGACaCCTACAGTGGCAGTCAGGTACGTcCGGA
35-39	consensus	CGGcAATACATCcAcGTGCTGGACCCcCaGTGACaCCTACaGTGGCAGTCAGGTACGTcCGGA
SEQ ID NO:	Isolate	
35	DK12	184 GCAACcACCGcTTCGATACGCAGTCATcGTGGACCTGcTAGTGGCGCGGGCCcACGATGTGCT
36	HK10	184 GCAACcACCGcTTCGATACGCAGTCATcGTGGACCTGcTAGTGGCGCGGGCCcACGATGTGCT
37	S2	184 GCAACcACCGcTTCGATACGCAGTCATcGTGGACCTATtGTGGCGCGGGCCcACtATGTGCT
39	S54	184 GCAACcACCGcTTCGATACGCAGTCATcGTGGACCTATtGTGGCGCGGGCCcACGCTGTGCT
38	S52	184 GCAACcACCGcTTCGATACGCAGTCATcGTGGACCTATtGTGGCGCGGGCCcACGCTGTGCT
35-39	consensus	GCAACcACCGcTTCGATACGCAGTCATcGTGGACCTATtGTGGCGCGGGCCcACgATGTGCT

FIGURE 1E-3

SEQ ID NO:	Isolate	
35	DK12	245 CTGCGCTCTACGTGGGtGATgTGTGTGGGGCCGTCTTCTtGTGGGACAAAGCCCTTCACGTT
36	HK10	245 CTGCGCTCTACGTGGGcGATAgTGTGGGGCCGTCTTCTCGTGGGACAAAGCCCTTCACGTT
37	S2	245 CTGCGCTCTACGTGGGTGAATgTGTGGGGCCGTCTTCTCGTGGGACAAAGCCCTTCACGTT
39	S54	245 CTGCGCTCTATGTGGGTGAATgTGTGGGGCCGTCTTCTCGTGGGACAAAGCCCTTCACGTT
38	S52	245 CTGCGCTCTATGTGGGTGAATgTGTGGGGCCGTCTTCTCGTGGGACAAAGCCCTTCACGTT
35-39	consensus	CTGCGCTCTAcGTGGGtGATaTGTGTGGGGCCGTCTTtCTcGTGGGACAAAGCCCTTCACGTT
35	DK12	306 CAGACctCGTCGCCCATCAAACaGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCAtCTT
36	HK10	306 CAGACcgcGTGCCCATCAAACCGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCAcCTT
37	S2	306 CAGACCTCGTCGCCCATCAAACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCATCTT
39	S54	306 CAGACCTCGTCGCCCATCAAACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCATCTT
38	S52	306 CAGACCTCGTCGCCCATCAAACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCATgTT
35-39	consensus	CAGACctCGTCGCCCATCAAACgGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCAtcTT

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

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REPLACEMENT SHEET

FIGURE 1E-4

SEQ ID NO:	Isolate	
35	DK12	367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
36	HK10	367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
37	S2	367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
39	S54	367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
38	S52	367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
35-39	consensus	TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
428	DK12	428 TaGGCGACGTCCTGCGTcTGCCCCCAGACCTTGTTCGACATAATAGctGGGGCCCCATTGGGG
36	HK10	428 TGGCGCACGTCCTGCGgTTGCCCCCAGACCTTGTTCGACATAATAGcCGGGCCCCATTGGGG
37	S2	428 TGGCGCACGTCCTGCGtTTGCCCCCAGACCGTGTTCGACATAATAGcCGGGCCCCATTGGGG
39	S54	428 TGGCGCACATCCTGCGATTGCCCCCAGACCTTGTTCGACATACTGGcCGGGCCCCATTGGGG
38	S52	428 TGGCGCACATCCTGCGATTGCCCCCAGACCTTGTTCGACATACTGGcCGGGCCCCATTGGGG
35-39	consensus	TGGCGCACgTcCTGGCG-tTGCCCCCAGACCTTGTTCGACATAaTaGcCGGGCCCCATTGGGG

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

Bukh et al.

Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

FIGURE 1E-5

SEQ ID NO:	Isolate	
35	DK12	489 CATCaTGGCGGGCCTAGCCTATTACTCCATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
36	HK10	489 CATCTTGGCaGGCCTAGCCTATTACTCCATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
37	S2	489 CATCTTGGCGGGCCTAGCCTATTACTCCATGCaAGGCAACTGGGCCAAGGTCGCTATCATC
39	S54	489 CATCTTGGCGGGCCTAGCCTATTACTCCATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
38	S52	489 CATCTTGGCGGGCCTAGCCTATTACTCCATGCAGGGCAACTGGGCCAAGGTCGCTATCgTC
35-39	consensus	CATCtTGGCgGGCCTAGCCTATTAcTCcATGCAGGGCAACTGGGCCAAGGTCGCTATcaTC
550	DK12	ATGGTTATGTTTTTCAGGaGTCGATGCC
550	HK10	ATGGTTATGTTTTTCAGGGGTGCGATGCC
550	S2	ATGGTTATGTTTTTCAGGGGTGCGAcGCC
550	S54	ATGATTATGTTTTTCAGGGGTGCGATGCC
550	S52	ATGATTATGTTTTTCAGGGGTGCGATGCC
550	consensus	ATGgTTATGTTTTTCAGGgGTCGAtGCC

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FIGURE 1F-1

SEQ ID NO:	Isolate
43	Z7
42	Z6
42-43 consensus	(Z6)
1	GTAACTATCaCAATGCCTCGGGCGTCTATCAGtTCACCAACGACTGCCCGAACTCGAGCA
1	GTAACTATCGCAATGCCTCGGGCGTCTATCAGCTCACCAACGACTGCCCGAACTCGAGCA
62	TAAATGTATAGGCCGAACACCAACATCCTACACCTCCAGGGTGCCTACCTGTGTGAGGGA
62	TAGTGTATAGGCCGAACACCAAGATCTTACACCTCCAGGGTGCtTgCCCTGTGTGAGGGT
42-43 consensus	(Z6)
123	GGGAACCACTCACGCTGCTGGGTGGCCCTTACTCCACCGTGGCGGcGcCTTATATCGGT
123	tGGGAAtCACTCACGCTGCTGGGTGGCCCTTACTCCCAACGTTGGCGGtGtCTTATATCGGT
42-43 consensus	(Z6)
184	GCACCGCTTGAAATCCaTCCGGAGACATGTGGACCTGATGGTAGGCGctGCTACaGTGTGCT
184	GCTCCGCTTGACtCCcTCCGGAGACATGTGGACCTGATGGTGGCGCGCTACTGTaTGCT
42-43 consensus	(Z6)
245	CcGCTCTCTACaTtTGGGACCTGTGCGGTGGcGtATTtTTGGTTGGtCAGATGTTtTCCTTT
245	CtGCCCTCTACGtTTGGAGAtCTGTGCGGTGGTGCAtTTCTTGGTTGGcCAGATGTTCTCCTT
42-43 consensus	(Z6)
43	Z7
42	Z6
42-43 consensus	(Z6)
43	Z7
42	Z6
42-43 consensus	(Z6)

FIGURE 1F-2

<u>SEQ ID NO:</u> 43	<u>Isolate</u> Z7	306 CCAGCCGCGACGCCACTGGACTAGCAGGACTGCAATTGTTCCATCTATGCgGGGCAcgtTt
42	Z6	306 CCAGCCGCGACGCCACTGGACTAGCAGGACTGCAATTGTTCTATCTAGCAGGGCATATC
42-43 consensus (Z6)		CCAGCCGCGACGCCACTGGACTAGCAGGACTGCAATTGTTCTATCTAGCAGGGCAtaTc
<u>SEQ ID NO:</u> 43	<u>Isolate</u> Z7	367 ACaGGCCACAGaATGGCATGGACATGATGAACTGGAGTCCCAACACCCTTgTCC
42	Z6	367 ACgGGCCACAGgATGGCATGGACATGATGAACCTGGAGTCCCAACACCCTTgTc
42-43 consensus (Z6)		ACgGGCCACAGgATGGCATGGACATGATGAACCTGGAGTCCCAACACCCTTgTc
<u>SEQ ID NO:</u> 43	<u>Isolate</u> Z7	428 TCGCCcAGGTtATGAGGATCCCTAGCACTCTGGTgGACCTACTCaCTGGAGGGCACTGGGG
42	Z6	428 TCGCCcAGGTtATGAGGATCCCTAGCACTCTGGTgATCTACTCGCTGGAGGGCACTGGGG
42-43 consensus (Z6)		TCGCCcAGGTtATGAGGATCCCTAGCACTCTGGTgATCTACTCGCTGGAGGGCACTGGGG
<u>SEQ ID NO:</u> 43	<u>Isolate</u> Z7	489 taTcCTTaTcGGGgTGGCaTACTTctGCATGCAAGCTAATTTGGGCCAAGGTCAttCTGGTC
42	Z6	489 CgTcCTTgTTGGGtTGGCGTACTTCAGtATGCAAGCTAATTTGGGCCAAaGTCACTCTGGTC
42-43 consensus (Z6)		cgTcCTTgTtGGGtTGGCGTACTTCaGtATGCAAGCTAATTTGGGCCAAaGTCACTCTGGTC
<u>SEQ ID NO:</u> 43	<u>Isolate</u> Z7	550 CTTTTCCCTCTaCGCTGGAGTTGATGCC
42	Z6	550 CTTTTCCCTCTTCGCTGGAGTTGATGCC
42-43 consensus (Z6)		CTTTTTCCCTCTcCGCTGGAGTTGATGCC

FIGURE 1G-1

SEQ ID NO:	Isolate	
45	SA1	1 GTtCCCTACCGgAATGCCTCTGGGGTTTAcCATGTcACCAATGAcTGCCCAAACTCcTCCA
47	SA5	1 GTCCCTACCGAAATGCCCTCTGGGGTTTATCATGTcACCAATGATTGCCCAAACTCTTCCA
49	SA7	1 GTCCCTACCGAAATGCCCTCcGGGGTTTATCATGTcACCAATGATTGCCCGAACTCTTCCA
46	SA4	1 GTTCCCTACCGAAAcGCCCTCTGGGGTTTATCATGTcACCAATGATTGCCCAAACTCTTCCA
50	SA13	1 GTTCCCTACCGAAATGCCCTCTGGGGTTTATCATGTcACCAATGATTGCCCAAACTCTTCCA
48	SA6	1 GTTCCCTACCGgAATGCCTCTGGGGTgTATCATGTtACCAATGATTGCCCAAACTCTTCCA
45-50	consensus	GTtCCcTACCGgAATGCCTCtGGGGTtTATcATGTcACCAATGAcTGCCCAAACTCtTCCA
45	SA1	62 TAGTCTACGAGGCTGATAgCCTGATctTGcACGCACcCTGGcTGCGTGCCCTGTGTcAGGcA
47	SA5	62 TAGTCTACGAGGCTGATAAcCTGATtCTGcACGCACcCTGGTTGCGTGCCCTGTGTcAaGgA
49	SA7	62 TAGTCTAtGAGGCTGAcAAcCTGATCCTTGcACGCACcCTGGTTGCGTGCCCTGTGTcAGaCA
46	SA4	62 TAGTtTACGAGGCTGATAAcCTGATCTTGcATGCACcCTGGTTGCGTGCCcTGTGTcAGGCA
50	SA13	62 TcGTCTACGAGGCTGATGACCTGATCTTAcACGCACcCTGGTTGCGTGCCCTGTGTtAGGCA
48	SA6	62 TagTCTAtGAGGCTGATGACCTGATCcTAcACGCACcCTGGcTGCGTGCCCTGTGTtccGGaA
45-50	consensus	TagTcTAcGAGGCTGAtaaCCTGATc-TgCAcGCACcCTGGtTGCGTGCCcTGTGTcaggcA

FIGURE 1G-2

SEQ ID NO:	Isolate	
45	SA1	123 AGaTAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACacTGTcAGCCCCGAcCtTCGGA
47	SA5	123 AGgTAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACaTTGTcAGCCCCGAAcCtTCGGA
49	SA7	123 AaATAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACaTTGTcAGCCCCGAAcCtTCGGA
46	SA4	123 AGaTAATGTCAGTAaGTGCTGGGTCCAAATCACCCCCACgTTGTcAGCCCCGAAcTTCGGA
50	SA13	123 GGgTAATGTCAGTAGGTGCTGGGTCCAgATCACCCCCACaCTGTcAGCCCCGAGcCtTCGGA
48	SA6	123 GGaTAATGTCAGTAGaTGCTGGGTtCaTATCACCCCCACACTaTCAGCCCCGAGcCtTCGGA
45-50	consensus	agaTAATGTCAGTAGgTGCTGGGTcCaaATCACCCCCACa -TgTCAGCCCCGAAccTTCGGA
45	SA1	184 GCGGTcACGGCTCCTCTTCGGAGGGcCGTTGACTACTTAGCGGGAGGaGCTGCTCTCTGCT
47	SA5	184 GCGGTcACGGCTCCTCTTCGGAGGGtCGTTGACTACTTAGCGGGAGGGGCTGCCCTCTGCT
49	SA7	184 GCGGTcACGGCTCCTCTTCGGAGGGCCGTTGACTACcTAGCGGGAGGGGCTGCCCTCTGCT
46	SA4	184 GCGGTcACGGCTCCTCTTCGGAGGGCCGTTGACTACTTAGCGGGAGGGGCTGCCCTCTGCT
50	SA13	184 GCGGTcACGGCTCCTCTTCGGAGGGCCGTTGACTACTTAGCGGGgGGGCTGCCCTtTGCT
48	SA6	184 GCGGTcACGGCTCCTCTTCGGAGGGCCGTTGATtTACTTgCGGGaGGGGCCGCCCTgTGCT
45-50	consensus	GCGGTcACGGCTCCTCTTCGGAGGGcCGTTGAcTACTaTCGGGGaGGGgGtGCcCtTcTGCT

FIGURE 1G-3

SEQ ID NO:	Isolate	
45	SA1	245 CCGCACTATACGTCCGCGACCGCTGCGGGCAGTGTtTcTGGTAGGCCAAATGTTCAcCTA
47	SA5	245 CCGCACTATACGTCCGCGACCGCTGCGGGCAGTGTtTcTGGTAGGCCAAATGTTCAcCTA
49	SA7	245 CCGCgCTATACGTCCGCGACCGCTGCGGGCAGTGTtTcTGGTAGGCCAgATGTTCAgCTA
46	SA4	245 CCGCaCTATACGTCCGCGACCGCTGCGGGCAGTGTtTcTGGTAGGCCAAATGTTCAcCTA
50	SA13	245 CCGCGTTATACGTCCGAGACCGCTGCGGGCAGTGTtTcTGGTAGGTCAAATGTTCAcCTA
48	SA6	245 CCGCGTTATACGTCCGAGACGtGTGCGGGGCAtTGTtTcTGGTAGGTCAAATGTTCAcCTA
45-50	consensus	CCGC- cTATA CGTCCGGGACGcGTGCGGGGCAgTGtTtTcTGGTAGGcCAaATGTTCAcCTA
45	SA1	306 TAGGCCTCGCCAGCATAcCaGTGCAGGACTGCAACTGTtTcTCCATTACAGtGGCCATATC
47	SA5	306 TAGGCCTCGCCAGCATAcTACGGTGCAGGACTGCAACTGTtTcTCCATTACAGcGGCCATATC
49	SA7	306 TAGGCCTCGCCAGCACACTACGGTGCAGGACTGCAACTGTtTcTCCATTACAGTGGCCATATC
46	SA4	306 TAGGCCTCGCCAGCACACTACGGTGCaaGACTGCAAtTgcTcTcATTACAGTGGCCATATC
50	SA13	306 TAGcCCTCGCCgGCATAaTgttGTGCAGGACTGCAACTGTtTcTCCATTACAGTGGCCAcATC
48	SA6	306 TAGgCCTCGCCCaGCATgcTaccgGTaCAGGACTGCAACTGcTCCATTACAGTGGCCATATC
45-50	consensus	TAGgCCTCGCCCaGCAtactaccgGTgCagGACTGCAAcTgtTCCATTACAGtGGCCATATC

FIGURE 1G-4

<u>SEQ ID NO:</u>	<u>Isolate</u>
45	SA1
47	SA5
49	SA7
46	SA4
50	SA13
48	SA6
45-50	consensus
367	ACCGGCCACCGgATGGcTtGGGACATGATGAATTGGTCACCTACGACAGCcTTGcTGA
367	ACCGGCCACCGAATGGcATGGcATGGGACATGATGAATTGGTCACCTACGACAGCcTTGGTGA
367	ACCGGCCACCGAATGGcATGGGACATGATGAATTGGTCACCTACGACAGCcTTGGTGA
367	ACCGGCCACCGGATGGcATGGGACATGATGAATTGGTCACCTACGACgGCcTTGcTGA
367	ACCGGCCACCGGATGGcATGGGACATGATGAATTGGTCACCTACaACAGCcTTGGTGA
367	ACtGGCCACCGGATGGcATGGGACATGATGAATTGGTCACCCcgCgACAGCcTTGGTGA
428	TGGCCCAAGtTgCtTACGGATtCCCCAGtGGTGCATaGACATCATaGCCGGGGGCCACTGGGG
428	TGGCCCAAGtTgCtTACGGATtCCCCAaGTGGTCATtGACATCATtGCCGGGGGCCACTGGGG
428	TGGCCCAAGtTgCtTACGGATtCCCCAGTGGTGCATCGACATCATtGCCGGGGGCCACTGGGG
428	TGGCCCAAGtTgCtTACGGATtCCCCAGGTGGTGCATCGACATCATtGCCGGGGGCCACTGGGG
428	TGGCCCAAGtTgCtTACGGATtCCCCAGGTGGTGCATCGACATCATtGCCGGGGGCCACTGGGG
428	TGGCCCAaaTgCtTACGGATtCCCCAGGTGGTGCATCGACATCATtGCCGGGGGCCACTGGGG
45-50	consensus
428	TGGCCCAAGtTgCtTACGGATtCCCCAGtGGTGCATtGACATCATtGCCGGGGGCCACTGGGG

FIGURE 1G-5

SEQ ID NO:	Isolate	
45	SA1	489 GGCTTTGTTtGCCGcCGCATACTTtGGTCgGCCcAACTGGGCTAAGGTaGTCTGGTt
47	SA5	489 GGCTTTGTTcGCCCGtCGCATACTTCGCGTCAGCGGCTAACTGGGCTAAGGTtGTCTGGTC
49	SA7	489 GGCTTTGTTcGCCCGCGCATAATTTCGCGTCAGCGGCTAACTGGGCTAAGGTtGTCTGGTC
46	SA4	489 GGCTTTGTTtGCCCGCGCATAATTTCGCGTCAGCGGCTAACTGGGCTAAGGTtTaCTGGTC
50	SA13	489 GGCTTTGTTcGCCCGCGCATACTaCGCGTCGCGGCTAACTGGGCTAAGGTtGTCTGGTC
48	SA6	489 GGCTTTGTTcGCCCGCtGCATACTtCGCGTCGCGGCTAACTGGGCTAAGGTtGTCTGGTC
45-50	consensus	GGTCTTTGTTcGCCGccGCATACTtCGCGTC-GCGGCTAACTGGGCTAAGGTtGTCTGGTC
45	SA1	550 CTGTTtCTGTTTTCGGGGGTTCGATGGC
47	SA5	550 CTGTTTCTGTTTTCGGGGGTTCGATGGC
49	SA7	550 TTGTTTCTGTTTTCGGGGGTTCGATGCC
46	SA4	550 TTGTTTCTGTTTTCGGGGGTTCGATGCC
50	SA13	550 CTGTTTCTGTTTTCGGGGGTTCGATGCC
48	SA6	550 tTGTTTCTGTTTTCGGGGGTtGATGCC
45-50	consensus	-TGTTtCTGTTTTCGGGGGTtCGATGcc

FIGURE 1H-1

SEQ ID NO:	Genotype	
30-33	(IV/2b)	1 GTGGAAGTCAGgAAcATcAGTTctAGcTACTAcGCCACCAATGATGTCTCaAAcAaCAGCA
34	(2c)	1 GTGGAGGTCAAGGACACCGGGCAGCTCTATACATGCCGACCAACGATGTCTCCAACCTCTAGTA
26-29	(III/2a)	1 GcccAAGTGAagAACACCAgtaCaGcTAcATGGTGACCAACGACTGTCTCcaATGACAGCA
35-39	(V/3a)	1 cTAGAGTGGCGGAATacGTCTGGCCTCTATgTCTTcACCAACGACTGTCTCCAATAGCAGTA
9-25	(II/1b)	1 tAtGAaGTGcGCAACGTgTCCGGGgtgTaccAtGTcACgAAcAGATgTGCCTTAacTCGAGtA
1-8	(I/1a)	1 tACCAAGTgCGCAACTCcaCgGGgCTtTACCATGTcACCAATGATGTCCGAATTCAGTA
40	(4a)	1 GAGCACTACCGGAATGCTTCGGGCATCTATcACATcACCAATGATGTCCGAATTCAGTA
42-43	(4c)	1 GTtAACTATcGCAATGCCTCGGGCGTCTATcACgTcACCAACGACTGCCCGAACTCGAGCA
44	(4d)	1 TACAACTATCGCAACAGCTCGGGTGTCTACCATGTcACCAACGACTGCCCGAACTCGAGCA
41	(4b)	1 GTGCACTACCGGAATGCTTCGGGCGTCTATcATGTcACCAATGATGTGCCCTTAACACcAGCA
45-50	(5a)	1 GTtCCcTACCGGAaATGCCTcTGGGgtTATcATGTcACCAATGATGTCCCAAACTCTTCCA
51	(6a)	1 CTTACCTACGGCAACTCCAGTGGGCTATACCATCTcACAAATGATGTCCCAAACTCCAGCA
1-51	consensus	A TA AC AA GA TG C AA
SEQ ID NO:	Genotype	
30-33	(IV/2b)	62 TCACCTGGCaactCACCaACGCAGTtCTCCACCTTCcCGGATCGTCCCaTGTGAGAATGA
34	(2c)	62 TCGTTTGGCAGCTTGaAGGAGCAGTGTCTcATACTCTGGATCGTCCCTTGTGAGCGTAC
26-29	(III/2a)	62 TCACcTGGCaactCcaAGCcCGGGTcCTCCACGTcCCCGGGTgtGTCCCGTGCgAGAAagt
35-39	(V/3a)	62 TtGTGTATGAGGCCGATGACGTcATTCTGCAcACACcTGGCTGTGTACCTTGTGTTCAGGA
9-25	(II/1b)	62 TtGTGTatGAGgCAGcGACaTGATcaTGCAcACcCCGGGTgGTgTCCCTGcGttCgGGGA
1-8	(I/1a)	62 TtGTGTACGAGcGcCGcGATgCcATcCTgCAcaCtCCgGGGTGTGTcCCTTGCgTTCGCGA
40	(4a)	62 TAGTCTATGAAGCTGACCATcACATCTTACACTTCCCGGGTGCCTACCTGTGTGTGATGAC
42-43	(4c)	62 TAGTGTATGAGGCCGAACACCAgATctTACACCTCCCGGATGCCTTgCCCTGTGTGAGGGT
44	(4d)	62 TAGTCTATGAaACCGATTACCACTTTACACCTCCCGGATGCCTTCCCTTGCgTGCAGGGA
41	(4b)	62 TAGTGTACGAGACGGAGCACCATcATGCACTTGCcAGGTGTGTCCCTGTGTGCGGAC
45-50	(5a)	62 TagTcTACGAGGCTGataaCCTGATctTgCAcGCACCTGGTTCGGTGCcCtGTGTcaggCA
51	(6a)	62 TCGTGTGGAGCGGATGCTATGATCTTGCATTTGCCTGGATGCTTGCCTTGTGTGTGAGGGT
1-51	consensus	T A T T CA CC GG TG T CC TG G

SEQ ID NO.	Genotype	1-51
30-33	(IV/2b)	CGGCCCTTGTATGTGGGAGACgTgTGCGGGGCGGTGATGATcGtGTGCGAGGCTtTCATAaT
34	(2c)	CTGCCCTTTATGTGGGGACGtGTGTGGCGCGGTGATGCTGGCGCGTCAAGTcGTGTCGT
26-29	(III/2a)	CcGctCTtTACGTGGGGACcTCTGCGGcGGGgTgATGTCTGCaGCCaGATgTTCATtGT
35-39	(V/3a)	CTGGCTCTACGTGGGTGATaTGTGTGGGCGGTCTTtCTcGTGGGACAAAGCCTTTCACGTT
9-25	(II/1b)	CCGcATGTACGTGGGgATcTcTGGGATcTcTGGGATcTcTGGTcTcTGGGcTGTTCACcctT
1-8	(I/1a)	CGGCCCTCTACGTGGGgATcTGTGGGCTGTCTTtCTtGTGgTcCaaCTGTTCACcctT
40	(4a)	CTGCCCTCTATGTGGGACCTCTGCGAGGTGCCCTTCTGTATGGGCGAGATGATCACTTT
42-43	(4c)	CtGCCCTCTACgTTGGAGATcTGTGCGGTGGtGcATTCTTGGTTGGcCAGATGTTcTcctT
44	(4d)	CCGCCCTCTACATCGGAGACGTGTGTGGGGTGTGTCTTGGTCTGCTCAACTGTTCACTT
41	(4b)	CCGCCCTCTACATTTGGAGATcTGTGTGGGCGGTCTCTCTAGTGGGCGAGCTGTTCCGACTT
45-50	(5a)	CCGcGcTATACGTGGGgACGcGTGCGGGGcAGTGTtTtTGGTAGGcCaaATGTTCAcCTA
51	(6a)	CATCCCTGTACATCGGGGACCTGTGTGGCTCTCTCTTGTGGGAGCAACTATTTCACTT
1-51	consensus	C T TA T GG GA TG GG T T CA T

SEQ ID NO.	Genotype	1-51
30-33	(IV/2b)	ATGCCCaGAACgCCaCaACTTtACCCaAGAGTGCAACTGTTCATCTACCAAGGTcatATC
34	(2c)	GTGCCaCAACACCATACGTTTGTCCAGGAATGCAACTGTTCATATACCGGGCGGCATT
26-29	(III/2a)	CTGCCGCaCaCaCACTgTtTGTGCaAGaATGCAATGTCTCcaTcTACCTGGtACCATC
35-39	(V/3a)	CAGACCTCGTCCCATCAACgTCCAGACCTGTAACTGCTCGTGTACCCAGGCCATcCTT
9-25	(II/1b)	cTcGcCTcGcCgGcAtgaGACagtaCAGgAcTgCAAcTcAAcTcTATCCcGgCacgTa
1-8	(I/1a)	cTctCCcAGgCgCaCTGGACaACGCaAGaCTGcAAATGTTCtATCTATCCcGGCCATATa
40	(4a)	TCGGCCGCTCGCCACTGGACCCAGCAGGAGTGCAATTTGTTCtATCTACGCaGGGCATATC
42-43	(4c)	CCAGCCGACGCCACTGGACTACGAGGACTGCAATTTGTTCtATCTACGCaGGGCATaTc
44	(4d)	CCAACCTCGCCGCCACTGGACCCACCCAGAGCTGCAATTTGTTCATCTACAGGACATATC
41	(4b)	CCGACCGCGCGGCACTGGACCCACCCAGGATTCaACTGCTCCATCTATCTCTGGTCACTG
45-50	(5a)	TAGcCTCGCCCaGCatacGgTgCAGGACTGCAAcTGTtTcATTACAGtGGCCATATC
51	(6a)	TCAGCCCGCGCTATGGACTGTGCAAGACTGCAACTGCTCCATCTATACAGGCCACGTC
1-51	consensus	CC C CA TG AA TG TC TTA GG T

FIGURE 1H-4

SEQ ID NO:	Genotype	
30-33	(IV/2b)	
34	(2c)	
26-29	(III/2a)	
35-39	(V/3a)	
9-25	(II/1b)	
1-8	(I/1a)	
40	(4a)	
42-43	(4c)	
44	(4d)	
41	(4b)	
45-50	(5a)	
51	(6a)	
1-51	consensus	
30-33	(IV/2b)	
34	(2c)	
26-29	(III/2a)	
35-39	(V/3a)	
9-25	(II/1b)	
1-8	(I/1a)	
40	(4a)	
42-43	(4c)	
44	(4d)	
41	(4b)	
45-50	(5a)	
51	(6a)	
1-51	consensus	

367	ACCGGCCACCGCATGGCaTGGGACATGATGCTAACTGGTCACCAACTCTtACCATGATCC	
367	ACGGGACACCGCATGGCTTGGGATATGATGAATGAATGGTCGCCCACTACCACTGCTCC	
367	ACTGgaCACCGTATGGCATGGGacATGATGATGAATGGTCGCCCACTACCACTGATCC	
367	TCAGGACATCGaATGGCTTGGGATATGATGATGAATGGTCGCCCACTACCACTGATGG	
367	tCAGGTcACCGcATGGcTGGGATATGATGATGAATGGTCGCCCACTACCACTGATGG	
367	ACGGGtCACCGcATGGcTGGGATATGATGATGAATGGTCGCCCACTACCACTGATGG	
367	ACGGGcCACAGGATGGCGTGGGACATGATGATGAATGGAGCCCTACCACTCTGCTCC	
367	ACgGGCCACAGgATGGCATGGGACATGATGATGAATGGAGCCCTACCACTGCTTc	
367	ACAGGACACAGaATGGCTTGGGACATGATGATGAATGGAGCCCTACCACTGCGACGCTGGTCC	
367	TCGGGCCACAGGATGGCTTGGGACATGATGATGAATGGAGCCCTACCACTGCGACGCTGGTCC	
367	ACcGGCCACCGgATGGCaTGGGACATGATGATGAATGGTCACCTaCgACaGCCcTTGgTGA	
367	ACCGGCCACAGGATGGCTTGGGACATGATGATGAATGGTCACCTaCgACaGCCcTTGgTGA	
	C GG CA G ATGGC TGGGA ATGATG T AA TGG CC C T T	
428	TGGCTATGCCGCTCGTGTtCCTGAGCTAGtCCTtGAAgTtGTCTTCGGcGGcCAATTGGGG	
428	TGGCGTACTTGGTGGCATCCCGGAAGTCATCTTGGATATTGTTACAGGAGTCAATTGGGG	
428	TGGCGTACGcGATGGCGGTTCGGAGGTcATCaTAGACATCaTtaGCGGgGCTCACTGGGG	
428	TgGGCACgTcCTGGGtTGGCCCGAGACCTTGTTCGACATaATaGcGGGGCCCAATTGGGG	
428	TaTGGCagTtTaCTCCGgATCCCaCAAGCTgTcGTGGAcATGGTgGgGgGCGCCCACTGGGG	
428	TaGCTCAGCTGTCTcGGaTCCCGCaAGCCaTCTTGGAcATGATCGCTGGTgCCcCACTGGGG	
428	TCGCCCAGATCATGAGGTCGCCcACAGCCCTTCTCGACATGGTTCGGGAGGCCCACTGGGG	
428	TCGCCCAGGTcATGAGGATCCCTAGCACTCTGGTaGATCTACTcGTGGAGGGCACTGGGG	
428	TCGCCCAACTTATGAGGATCCCGAGGCCCATGCTCGACCTGCTTCAGCGGGCCCACTGGGG	
428	TGGCTCAGATCTTACGGATCCCTCTATCTAGGTGACTTGTCTACCGGGGGTCACTGGGG	
428	TGGCCCAgTtGCTACGGATtCCCGAGTGGTCATtGACATCATtGCCGGGGGCCACTGGGG	
428	TATCTAGCATCTTGGGGTACCTGAGATTtTGGGAGTGTGATATTGGTGGCCCACTGGGG	
	T C G T CC T T GG G CA TGGG	

FIGURE 1H-5

SEQ ID NO.	Genotype
30-33	(IV/2b)
34	(2c)
26-29	(III/2a)
35-39	(V/3a)
9-25	(II/1b)
1-8	(I/1a)
40	(4a)
42-43	(4c)
44	(4d)
41	(4b)
45-50	(5a)
51	(6a)

[illegible]

SEQ ID NO:	Genotype
30-33	(IV/2b)
34	(2c)
26-29	(III/2a)
35-39	(V/3a)
9-25	(II/1b)
1-8	(I/1a)
40	(4a)
42-43	(4c)
44	(4d)
41	(4b)
45-50	(5a)
51	(6a)

1-51
consensus
T T T C GG GT GA G

FIGURE 2A-1

SEQ ID NO:	Isolate	
56	S14	1 YQVRNSTGLYHVTNDCPNSSIVYEADAILHaPGCVPCVREGNtSRCWAMTPTVATRDGK
52	DK7	1 YQVRNSTGLYHVTNDCPNSSIVYEADAILHTPGCVPCVREGNvSRCWAMTPTVATRDGK
59	US11	1 YQVRNSTGLYHVTNDCPNSSIVYEADAILHTPGCVPCVREGNaSRCWAMTPTVATRDGK
55	DR4	1 HQVRNSTGLYHVTNDCPNSSIVYEADAILHTPGCVPCVREGNtSRCWAVTPTVATRDGK
54	DR1	1 HQVRNSTGLYHVTNDCPNSSIVYEADAILHaPGCVPCVREGNASRCWAVTPTVATRDGK
53	DK9	1 YQVRNSSGLYHVTNDCPNSSIVYEADAILHSPGCVPCVREGNASKCWAVAPTATRDGK
58	SW1	1 YQVRNSSGLYHVTNDCPNSSIVYEADAILHSPGCVPCVREGdApKCWAVAPTATRDGK
57	S18	1 YQVRNSTGLYHVTNDCPNSSIVYEADtILHSPGCVPCVREGnAsrCWvpVAPTATRDGK
52-59	consensus	YQVRNSTGLYHVTNDCPNSSIVYEaDaILH- PGCVPCVREGnaSrCWvavtPTVATRDGK
56	S14	62 LPatQLRRyIDLLVGSATLCSALYVGDLGCVFLVQLFTFSPrRLWTTQdCNCsIYPGHI
52	DK7	62 LPTaQLRRHIDLLVGSATLCSALYVGDLGCVFLVQLFTFSPrRHWTtQGCNCsIYPGHI
59	US11	62 LPTTQLRRHIDLLVGSATLCSALYVGDLGCVFLVQLFTFSPrRHWTtQGCNCsIYPGHI
55	DR4	62 LPTTQLRRHIDLLVGSATLCSALYVGDLGCVFLVQLFTFSPrhHWTtQdCNCsIYPGHI
54	DR1	62 LPTTQLRRHIDLLVGSATLCSALYVGDLGCVFLVQLFTFSPrRHWTtQdCNCsIYPGHI
53	DK9	62 LPATQLRRHIDLLVGSATLCSALYVGDLGCVFLVQLFTFSPrRHWTtQdCNCsIYPGHI
58	SW1	62 LPATQLRRHIDLLVGSATLCSALYVGDLGCVFLVQLFTFSPrRHWTtQdCNCsIYPGHI
57	S18	62 LPATQLRRHIDLLVGSATLCSALYVGDLGCVFLVQLFTiSPRRHWTtQdCNCsIYPGHI
52-59	consensus	LP-tQLRRhIDLLVGSATLCSALYVGDLGCVFLVgQLFTfSPRrhWTtQdCNCsIYPGHI

FIGURE 2A-2

SEQ ID NO:	Isolate		
56	S14	123	TGHRMAWDMMNWSPPTTALVVAQLLRIPQAiLDMiAGAHGVLAGIAYFSMvGNWAKVLvV
52	DK7	123	TGHRMAWDMMNWSPPTTALVVAQLLRIPQAiLDMiAGAHGVLAGIAYFSMvGNWAKVLvV
59	US11	123	TGHRMAWDMMNWSPPTaALVVAQLLRIPQAiLDMiAGAHGVLAGIAYFSMvGNWAKVLvV
55	DR4	123	TGHRMAWDMMNWSPPTTALVVAQLLRIPQAiLDMiAGAHGVLAGIAYFSMvGNWAKVLvV
54	DR1	123	TGHRMAWDMMNWSPPTTALVMAQLLRIPQAiLDMiAGAHGVLAGIAYFSMvGNWAKVvVv
53	DK9	123	TGHRMAWDMMNWSPTaALVMAQLLRIPQAiLDMiAGAHGVLAGIAYFSMvGNWAKVvVv
58	SW1	123	TGHRMAWDMMNWSPPTTALVvAQLLRIPQAiLDMiAGAHGVLAGIAYFSMvGNWAKVLiV
57	S18	123	TGHRMAWDMMNWSPPTALViAQLLRvPQAiLDMiAGAHGVLAGIAYFSMaGNWAKVLiV
52-59	consensus		TGHRMAWDMMNWSPPTaALVvAQLLRiPQAiLDMiAGAHGVLAGIAYFSMvGNWAKVLvV
SEQ ID NO:	Isolate		
56	S14	184	LLLFAgVDA
52	DK7	184	LLLFAgVDA
59	US11	184	LLLFAgVDA
55	DR4	184	LLLFAgVDA
54	DR1	184	LLLFAgVDA
53	DK9	184	LLLFAgVDA
58	SW1	184	LLLFAgVDA
57	S18	184	LLLFAgVDA
52-59	consensus		LLLFAgVDA

FIGURE 2B-1

SEQ ID NO:	Isolate	
75	T10	1 YEVRNVSGmYHVTNDCSNSSIVYEaAdlIMHTPGCPCVREGNsSRCWVALTPTLAARntS
62	DK1	1 YEVRNVSGvYHVTNDCSNSSIVYEaVdIMHTPGCPCVRENNhSRCWVALTPTLAARNAS
64	HK4	1 hEVhNVSGiYHVTNDCSNSSIVYEaAdMIMHTPGCPCVRENNSSRCWVALTPTLAARNAS
76	US6	1 YEVRNVSGmYHVTNDCSNSSIVYEaAdMIMHTPGCPCVRENNSSRCWVALTPTLAARNAS
68	IND8	1 YEVRNVSGvYHVTNDCSNSSIVYEaAdMIMHTPGCPCVREGNfSsCWVALTPTLAARNAS
67	IND5	1 YEVRNVSGvYHVTNDCSNSSIVYEaAdMIMHTPGCPCVREGNSRCWVALTPTLAARNAS
73	SW2	1 YEVRNVSGvYHVTNDCSNSSIVYEaAdMIMHTPGCPCVREaNSRCWVALTPTLAARntS
63	HK3	1 YEVRNVSGiYHVTNDCSNSSvVYEaDmIMHTPGCPCVRENNSSRCWVALTPTLAARNVS
66	HK8	1 YEVRNVSGiYHVTNDCSNSSIVYEaDmIMHTPGmPCVRENNSSRCWVALTPTLAARNVS
61	D3	1 YEVRNVSGvYqVTNDCSNSSIVYEaDmIMHTPGCPCVREDnSSRCWVALTPTLAARNsS
74	T3	1 YEVRNVSGvYVTNDCSNSSIVYEaDmIMHTPGCPCVRESnSSRCWVALTPTLAARNAS
65	HK5	1 YEVRNVSGvYHVTNDCSNlSIVYEtdMIMHTPGCPCVRENNSSRCWVALaPTLAARNAS
71	S45	1 YEVRNVSGaYHVTNDCSNSSIVYEaVdIlHTPGCPCVRENNSSRCWVALTPTLAARNSS
72	SA10	1 YEVRNVSGmYHVTNDCSNSSIVYEaAdMIMHTPGCPCVRENNSSRCWVALTPTLAARNSS
69	P10	1 YEVRNVSGvYHVTNDCSNSSIVYEaAdMIMHTPGCPCVRENNSSRCWVALTPTLAARNSS
60	D1	1 YEVRNVSGvYHVTNDCSNSSIVYEtdADMIMHTPGCPCVREDnSSRCWVALTPTLAARNgn
70	S9	1 YEVRNVSGaYHVTNDCSNSSIVYEaAdVIMHTPGCPCVqEgNssqCWVALTPTLAARNat
60-76	consensus	YEVRNVSGvYhVTNDCSNSSiVYEaAdmImHTPGCPCVrEnNssrCWVALtPTLAARNas

FIGURE 2B-2

SEQ ID NO:	Isolate	
75	T10	62 vPTTTIRRHVDLLVGAAAFCSAMVVDLCGSVFLVSQVLTFTSPRRHET1QDCNCISIYPGHI
62	DK1	62 IPTTTIRRHVDLLVGAAAFCSAMVVDLCGSVFLVSQVLTFTSPRRHETaQDCNCISIYPGHV
64	HK4	62 IPTTTIRRHVDLLVGAAAFCSAMVVDLCGSVFLVSQVLTFTSPRRHETVQDCNCISIYPGHV
76	US6	62 VPTTTIRRHVDLLVGAAtFCSAMVVDLCGSVFLVSQVLTFTSPRqHETVQDCNCISIYPGHV
68	IND8	62 VPTTTIRRHVDLLVGAAAFCSAMVVDLCGSVFLVSQVLTFTSPRRHETVQDCNCISIYPGHV
67	IND5	62 VstTTIRRHVDLLVGAAAFCSAMVVDLCGSVFLVSQVLTFTSPRRHETVQDCNCISIYPGHV
73	SW2	62 VPTTTIRRHVDLLVGAAAFCSvMYVVDLCGSVFLVSQVLTFTSPRRHETVQDCNCISIYPGHV
63	HK3	62 VPTTTIRRHVDLLVGAAAFCSAMVVDLCGSVFLVSQVLTFTSPRRHETVQDCNCISIYPGHV
66	HK8	62 VPTTTIRRHVDLLVGAAAFCSAMVVDLCGSVFLVSQVLTFTSPRRHETVQDCNCISIYPGHV
61	D3	62 VPTTTIRRHVDLLVGAAAFCSAMVVDLCGSVFLVSQVLTFTSPRRHETVQeCNCISIYPGHV
74	T3	62 VPTktIRRHVDLLVGAAAFCSAMVVDLCGSVFLVSQVLTFTSPRRHETVQDCNCISIYPGHV
65	HK5	62 VPTTaIRRHVDLLVGAAAFCSAMVVDLCGSVFLVSQVLTFTSPRRHETVQDCNCISIYPGHV
71	S45	62 VPTTTIRRHVDLLVGAAAFCSAMVVDLCGSVFLVSQVLTFTSPRRHETVQDCNCISIYPGHV
72	SA10	62 VPTTTIRRHVDLLVGAAAFCSAMVVDLCGSVFLVSQVLTFTSPRRyETVQDCNCISIYPGrV
69	P10	62 VPTTAIRRHVDLLVGAAAFCSAMVVDLCGSVLLVSQVLTFTSPRRHwTVQDCNCISIYPGHV
60	D1	62 VPTTAIRRHVDLLVGAAAFCSAMVVDLCGSVFLISQVLTFTSPRRHETVQeCNCISIYPGHV
70	S9	62 VPTTtIRRHVDLLVGAAAFCSAMVVDLCGSVFLISQVLTFTSPRRHETVQnCNCISIYPGHV
60-76	consensus	vpTttIRRHVDLLVGAAAFCSAMVVDLCGSVFLVSQVLTFTSPRRhetVQdCNCISIYPGhv

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FIGURE 2B-3

SEQ ID NO:	Isolate	
75	T10	123 SGRMAWDMNMNWSPTTALVVSQLLRIPQAVmDMVtGAHWGVLAGLAYYSMAGNWAkVLIV
62	DK1	123 SGRMAWDMNMNWSPTTALVVSQLLRIPQAVvDMVAGAHGVLAGLAYYSMAGNWAkVLIV
64	HK4	123 SGRMAWDMNMNWSPTAALVVSQLLRLPQAVMDMVAGAHGVLAGLAYYSMVGNWAkVLIV
76	US6	123 SGRMAWDMNMNWSPTAALVVSQLLRIPQAVMDMVAGAHGVLAGLAYYSMVGNWAkVLIV
68	IND8	123 SGRMAWDMNMNWSPTAALVVSQLLRIPQAVMDMVAGAHGVLAGLAYYSMVGNWAkVLIV
67	IND5	123 SGRMAWDMNMNWSPTAALVVSQLLRIPQAVMDMVAGAHGVLAGLAYYSMVGNWAkVLIV
73	SW2	123 SGRMAWDMNMNWSPTAALVVSQLLRIPQAVMDMVAGAHGVLAGLAYYSMVGNWAkVLIV
63	HK3	123 SGRMAWDMNMNWSPTAALVVSQLLRIPQAVMDMVAGAHGVLAGLAYYSMVGNWAkVLIV
66	HK8	123 SGRMAWDMNMNWSPTAALVVSQLLRIPQAVMDMVAGAHGVLAGLAYYSMVGNWAkVLIV
61	D3	123 TGRMAWDMNMNWSPTAALVVSQLLRIPQAVMDMVAGAHGVLAGLAYYSMVGNWAkVLIV
74	T3	123 TGRMAWDMNMNWSPTTALVVSQLLRIPQAVMDMVAGAHGVLAGLAYYSMVGNWAkVLIV
65	HK5	123 TGRMAWDMNMNWSPTTALVVSQLLRIPQAVMDMVAGAHGVLAGLAYYSMVGNWAkVLIV
71	S45	123 TGRMAWDMNMNWSPTAALVVSQLLRIPQAVMDMVAGAHGVLAGLAYYSMVGNWAkVLIV
72	SA10	123 TGRMAWDMNMNWSPTAALVVSQLLRIPQAVMDMVAGAHGVLAGLAYYSMVGNWAkVLIV
69	P10	123 sGRMAWDMNMNWSPTAALVVSQLLRIPQAVMDMVAGAHGVLAGLAYYSMVGNWAkVLIV
60	D1	123 TGRMAWDMNMNWSPTTALVVSQLLRIPQAVMDMVAGAHGVLAGLAYYSMVGNWAkVLIV
70	S9	123 TGRMAWDMNMNWSPTTALVVSQLLRIPQAVMDMVAGAHGVLAGLAYYSMVGNWAkVLIV
60-76	consensus	SGRMAWDMNMNWSPTAALVVSQLLRIPQAVvDmVaGAHWGVLAGLAYYSMVGNWAkVLIV

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FIGURE 2B-4

<u>SEQ ID NO:</u>	<u>Isolate</u>	
75	T10	184 mLLFAGVDG
62	DK1	184 1LLFAGVDG
64	HK4	184 mLLFAGVDG
76	US6	184 1LLFAGVDG
68	IND8	184 MLLFAGVDG
67	IND5	184 MLLFAGVDG
73	SW2	184 MLLFAGVDG
63	HK3	184 MLLFAGVDG
66	HK8	184 MLLFAGVDG
61	D3	184 MLLFAGVDG
74	T3	184 1LLFAGVDG
65	HK5	184 MLLFAGVDG
71	S45	184 MLLFAGVDG
72	SA10	184 MLLFAGVDG
69	P10	184 MLLFAGVDG
60	D1	184 MLLFAGVDG
70	S9	184 MLLFAGVDG
60-76	consensus	mLLFAGVDG

FIGURE 2C-1

SEQ ID NO:	Isolate	
77	T2	1 A QVrNTsrGyMVTNDCSNeSITWQLQAAVLHVPGCIPCErLGNTSRCWIPVtPNVAVRQPG
78	T4	1 A QVKNttnSYMTNDCSNDsITWQLQAAVLHVPGCVPCeKtGNTSRCWIPVSPNVAVRQPG
79	T9	1 AeVKNtSTSYMTNDCSNDsITWQLQAAVLHVPGCVPCeRvGNASRCWIPVSPNVAVRQPG
80	US10	1 vqVKNtSTSYMTNDCSNDsITWQLeAAVLHVPGCVPCeKvGNTSRCWIPVSPNVAVRQPG
77-80	consensus	aqVKNtstSYMTNDCSNDsITWQLqAAVLHVPGCVPCe - vGNTSRCWIPVsPNVAV - - PG
SEQ ID NO:	Isolate	
77	T2	62 ALTQGLRTHIDMVMSATLCSALYVGDL CGGVMLAAQMFIVSPrrHwFVQeCNCsIYPGTI
78	T4	62 ALTQGLRTHIDMVMSATLCSALYVGDL CGGVMLAAQMFIVSPQHhWFVQdCNCsIYPGTI
79	T9	62 ALTQGLRTHIDMVMSATLCSALYVGDL CGGVMLAAQMFII SPQHhWFVQeCNCsIYPGTI
80	US10	62 ALTQGLRTHIDMVMSATLCSALYVGDF CGGmMLAAQMFIVSPrrHhsFVQeCNCsIYPGTI
77-80	consensus	ALTQGLRTHIDMVMSATLCSALYVGDL CGGVMLAAQMFIVSP - hHwFVQeCNCsIYPGTI
SEQ ID NO:	Isolate	
77	T2	123 TGHrMAWdMMMNWSPTaTmILAYaMRVPEVIIdIIGAHWGVMFGLAYFSMQGAWAKVVI
78	T4	123 TGHrMAWdMMMNWSPTaTmILAYaMRVPEVIIdIVSGAHWGVMFGLAYFSMQGAWAKVVI
79	T9	123 TGHrMAWdMMMNWSPTtTmILAYaMRVPEVIIdIISGAHWGMFGLAYFSMQGAWAKVVI
80	US10	123 TGHrMAWdMMMNWSPTaTlILAYvMRVPEVIIdIISGAHWGVL FGLAYFSMQGAWAKVVI
77-80	consensus	TGHrMAWdMMMNWSPTaTmILAYaMRVPEVIIdIISGAHWGMFGLAYFSMQGAWAKVVI

FIGURE 2C-2

<u>SEQ ID NO:</u>	<u>Isolate</u>	
77	T2	184 LLLAAGVDA
78	T4	184 LLLAAGVDA
79	T9	184 LLLtAGVDA
80	US10	184 LLLaAGVDA
77-80	consensus	LLLaAGVDA

FIGURE 2D-1

SEQ ID NO:	Isolate	
82	DK11	1 VEVNtSSSYATNDCSNnSITWQLTNAVHLPGVPCENDNGTLHCWIQVTPNAVKHGRG
83	SW3	1 VEVNtSSSYATNDCSNnSITWQLTNAVHLPGVPCENDNGTLHCWIQVTPNAVKHGRG
84	T8	1 VEVNtSfSYATNDCSNnSITWQLTNAVHLPGVPCENDNGTLRCWIQVTPNAVKHGRG
81	DK8	1 VEVNtSSSYATNDCSNnSITWQLTNAVHLPGVPCENDNGTLRCWIQVTPNAVKHGRG
81-84	consensus	VEVRN-SsSYATNDCSNnSITWQLTNAVHLPGVPCENDNGTL-CWIQVTPNAVKHGRG
SEQ ID NO:	Isolate	
82	DK11	62 ALTHNLRahIDMIvMAATVCSALYVGdVCGAVMIvSQAFIvSPEHhFTQECNCsIYQGHl
83	SW3	62 ALTHNLRahIDMIvMAATVCSALYVGdVCGAVMIvSQAFIvSPEHhFTQECNCsIYQGHl
84	T8	62 ALTHNLRThVDVIvMAATVCSALYVGdVCGAVMIaSQAFIISPERHNFTQECNCsIYQGHl
81	DK8	62 ALTHNLRThVDVIvMAATVCSALYVGdVCGAVMIvSQAlIISPERHNFTQECNCsIYQGHl
81-84	consensus	ALTHNLR-HvD-IVMAATVCSALYVGdVCGAVMIvSQAFIISPERHnFTQECNCsIYQGHl
SEQ ID NO:	Isolate	
82	DK11	123 TGHrMAWDMMLNWSPTLTmILAYAArVPELVLeVVFgGHGwVVFGLAYfSMQGAwAKVIAI
83	SW3	123 TGHrMAWDMMLNWSPTLTmILAYAArVPELVLeVVFgGHGwVVFGLAYfSMQGAwAKVIAI
84	T8	123 TGHrMAWDMMLNWSPTLTmILAYAArVPELVLeVVFgGHGwVVFGLAYfSMQGAwAKVIAI
81	DK8	123 TGHrMAWDMMLNWSPTLTmILAYAArVPELVLeVVFgGHGwVVFGLAYfSMQGAwAKVIAI
81-84	consensus	TGHrMAWDMMLNWSPTLTmILAYAArVPELVLeVVFgGHGwVVFGLAYfSMQGAwAKVIAI

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FIGURE 2D-2

<u>SEQ ID NO:</u>	<u>Isolate</u>	
82	DK11	184 LLLVAGVDA
83	SW3	184 LLLVAGVDA
84	T8	184 LLLVAGVDA
81	DK8	184 LLLVAGVDA
81-84	consensus	LLL VAGVDA

FIGURE 2E-1

SEQ ID NO:	Isolate	
86	DK12	1 LEWRNVSGLYVLTNDCsNSSIIVEADDDVILHTPGCVPCVQDGNSTCWTSTVTPTVAVRYVG
87	HK10	1 LEWRNVSGLYVLTNDCpNSSIIVEADDDVILHTPGCVPCVQDGNSTCWTSTVTPTVAVRYVG
88	S2	1 LEWRNTSGLYVLTNDCSNSSIIVEADDDVILHTPGCVPCVQDGNSTCWTPTPTVAVRYVG
90	S54	1 LEWRNTSGLYiLTNDCSNSSIIVEADDDVILHTPGCVPCVQDGNSTCWTPTPTVAVRYVG
89	S52	1 LEWRNTSGLYVLTNDCSNSSIIVEADDDVILHTPGCVPCVQDGNSTsmCWTPTPTVAVRYVG
86-90	consensus	LEWRNtSGLYvLTNDCsNSSIIVEADDDVILHTPGCVPCVQDGNSTtCWTpVTPTVAVRYVG
SEQ ID NO:	Isolate	
86	DK12	62 ATTASIRSHVDLLVGAATMCSALYVGdVCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
87	HK10	62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
88	S2	62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
90	S54	62 ATTASIRSHVDLLVGAATLCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
89	S52	62 ATTASIRSHVDLLVGAATLCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHv
86-90	consensus	ATTASIRSHVDLLVGAATmCSALYVGDMcGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL

FIGURE 2E-2

SEQ ID NO:	Isolate		
86	DK12	123	SGHRMAWDMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGIMAGLAYYSMQGNWAKVAIL
87	HK10	123	SGHRMAWDMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGILAGLAYYSMQGNWAKVAIL
88	S2	123	SGHRMAWDMMNWSPAVGMVVAHVLRLPQTVFDIIAGAHWGILAGLAYYSMQGNWAKVAIL
90	S54	123	SGHRMAWDMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGILAGLAYYSMQGNWAKVAIL
89	S52	123	SGHRMAWDMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGILAGLAYYSMQGNWAKVAIL
86-90	consensus		SGHRMAWDMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGILAGLAYYSMQGNWAKVAIL
SEQ ID NO:	Isolate		
86	DK12	184	MVMFSGVDA
87	HK10	184	MVMFSGVDA
88	S2	184	MVMFSGVDA
90	S54	184	MIMFSGVDA
89	S52	184	MIMFSGVDA
86-90	consensus		MVMFSGVDA

[illegible]

FIGURE 2G-1

SEQ ID NO:	Isolate	
98	SA5	1 VPYRNASGVVHVTNDPCNPSSIVYEADNLIILHAPGCVPCVkegNVSRCWVQITPTLSAPNLG
100	SA7	1 VPYRNASGVVHVTNDPCNPSSIVYEADNLIILHAPGCVPCVRQnNVSRCWVQITPTLSAPNLG
97	SA4	1 VPYRNASGVVHVTNDPCNPSSIVYEADNLIILHAPGCVPCVRQDNVskCWVQITPTLSAPNLG
96	SA1	1 VPYRNASGVVHVTNDPCNPSSIVYEADsLIILHAPGCVPCVRQDNVSRWVQITPTLSAPtfg
99	SA6	1 VPYRNASGVVHVTNDPCNPSSIVYEADDLIILHAPGCVPCVRkDNVSRWVhITPTLSAPSLG
101	SA13	1 VPYRNASGVVHVTNDPCNPSSIVYEADDLIILHAPGCVPCVRqgNVSRCWVqITPTLSAPSLG
96-101	consensus	VPYRNASGVVHVTNDPCNPSSIVYEADnLIILHAPGCVPCVrqnVsrCWVqITPTLSAPnlg
SEQ ID NO:	Isolate	
98	SA5	62 AVTAPLRRvVDYLAGGAALCSALYVGDA CGAVFLVGQMfTYRPRQHTTVQDCNCsIYSgHI
100	SA7	62 AVTAPLRRvVDYLAGGAALCSALYVGDA CGAVFLVGQMfTYRPRQHTTVQDCNCsIYSgHI
97	SA4	62 AVTAPLRRvVDYLAGGAALCSALYVGDA CGAVFLVGQMfTYRPRQHTTVQDCNCsIYSgHI
96	SA1	62 AVTAPLRRvVDYLAGGAALCSALYVGDA CGAVFLVGQMfTYRPRQHTTVQDCNCsIYSgHI
99	SA6	62 AVTAPLRRvVDYLAGGAALCSALYVGDA CGAVFLVGQMfTYRPRQHaTVQDCNCsIYSgHI
101	SA13	62 AVTAPLRRvVDYLAGGAALCSALYVGDA CGAVFLVGQMfTYsPRrHnvVQDCNCsIYSgHI
96-101	consensus	AVTAPLRRvVDYLAGGAALCSALYVGDA CGAVFLVGQMfTYrPRqHttVQDCNCsIYSgHI

FIGURE 2G-2

<u>SEQ ID NO:</u>	<u>Isolate</u>	
98	SA5	123 TGHMAWDMMNWSPPTTALVMAQVLRIPQVWIDIIAGGHGVLFAVAFASAANWAKVVLV
100	SA7	123 TGHMAWDMMNWSPPTTALVMAQVLRIPQVWIDIIAGGHGVLFAVAFASAANWAKVVLV
97	SA4	123 TGHMAWDMMNWSPPTTALLMAQLLRIPQVWIDIIAGGHGVLFAVAFASAANWAKVVLV
96	SA1	123 TGHMAWDMMNWSPPTTALLMAQMLRIPQVWIDIIAGGHGVLFAVAFASAANWAKVVLV
99	SA6	123 TGHMAWDMMNWSPaTALVMAQMLRIPQVWIDIIAGGHGVLFAVAFASAANWAKVVLV
101	SA13	123 TGHMAWDMMNWSPcTALVMAQLLRIPQVWIDIIAGaHWGVLFAAAyASAANWAKVVLV
96-101	consensus	TGHMAWDMMNWSPcTALVMAQLLRIPQVWIDIIAGgHWGVLFAaYfASAANWAKVVLV
98	Isolate SA5	184 LFLFAGVDg
100	SA7	184 LFLFAGVDA
97	SA4	184 LFLFAGVDA
96	SA1	184 LFLFAGVDg
99	SA6	184 LFLFAGVDA
101	SA13	184 LFLFAGVDA
96-101	consensus	LFLFAGVDA

FIGURE 2H-1

SEQ ID NO:	Genotype	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000	1001	1002	1003	1004	1005	1006	1007	1008	1009	1010	1011	1012	1013	1014	1015	1016	1017	1018	1019	1020	1021	1022	1023	1024	1025	1026	1027	1028	1029	1030	1031	1032	1033	1034	1035	1036	1037	1038	1039	1040	1041	1042	1043	1044	1045	1046	1047	1048	1049	1050	1051	1052	1053	1054	1055	1056	1057	1058	1059	1060	1061	1062	1063	1064	1065	1066	1067	1068	1069	1070	1071	1072	1073	1074	1075	1076	1077	1078	1079	1080	1081	1082	1083	1084	1085	1086	1087	1088	1089	1090	1091	1092	1093	1094	1095	1096	1097	1098	1099	1100	1101	1102	1103	1104	1105	1106	1107	1108	1109	1110	1111	1112	1113	1114	1115	1116	1117	1118	1119	1120	1121	1122	1123	1124	1125	1126	1127	1128	1129	1130	1131	1132	1133	1134	1135	1136	1137	1138	1139	1140	1141	1142	1143	1144	1145	1146	1147	1148	1149	1150	1151	1152	1153	1154	1155	1156	1157	1158	1159	1160	1161	1162	1163	1164	1165	1166	1167	1168	1169	1170	1171	1172	1173	1174	1175	1176	1177	1178	1179	1180	1181	1182	1183	1184	1185	1186	1187	1188	1189	1190	1191	1192	1193	1194	1195	1196	1197	1198	1199	1200	1201	1202	1203	1204	1205	1206	1207	1208	1209	1210	1211	1212	1213	1214	1215	1216	1217	1218	1219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SEQ ID NO:	Genotype	consensus
81-84	(IV/2b)	
85	(2c)	
77-80	(III/2a)	
86-90	(V/3a)	
60-76	(II/1b)	
52-59	(I/1a)	
91	(4a)	
93-94	(4c)	
95	(4d)	
92	(4b)	
96-101	(5a)	
102	(6a)	
52-102	consensus	

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SEQ ID NO:	Genotype	consensus
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60-76	(II/1b)	
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91	(4a)	
93-94	(4c)	
95	(4d)	
92	(4b)	
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102	(6a)	
52-102	consensus	

SEQ ID NO:	Genotype	consensus
81-84	(IV/2b)	
85	(2c)	
77-80	(III/2a)	
86-90	(V/3a)	
60-76	(II/1b)	
52-59	(I/1a)	
91	(4a)	
93-94	(4c)	
95	(4d)	
92	(4b)	
96-101	(5a)	
102	(6a)	
52-102	consensus	

SEQ ID NO:	Genotype	consensus
81-84		

Genotype	SEQ ID NO: 52-102	Isolate	yevrntsgv	thvTND	Cs	SS	iy	ea	ad	lit	PG	CP	CV	reg	tsr	cl	nav	pt	va	arn	ag	pt	tt	l	rh	vp	l	l	g	at	Cs	Sal	v	cd	Cs	sv	l								
IV/2b	82	DK11	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	83	SW3	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	84	DK8	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	85	T83	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	86	T83	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	87	T83	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	88	US10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	89	T9	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	90	T9	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	91	T2	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
(V)/3a	92	DK12	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	93	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	94	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	95	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	96	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	97	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	98	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	99	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	100	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	101	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
102	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV	
11/1b	92	DK12	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	93	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	94	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	95	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	96	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	97	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	98	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	99	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	100	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	101	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
102	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV	
11/1a	92	DK12	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	93	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	94	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	95	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	96	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	97	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	98	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	99	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	100	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
	101	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV
102	HK10	VEVRNTSS-YA	---S-n	IT	HL	TA	VL	-L	---	V	-	V	-	END	GT	LH	---	IQ	VT	-	NA	V	CH	R	GA	L	TH	RL	---	AH	-	MI	VA	-	TV	-	AL	-	V	-	V	-	AM	IV	

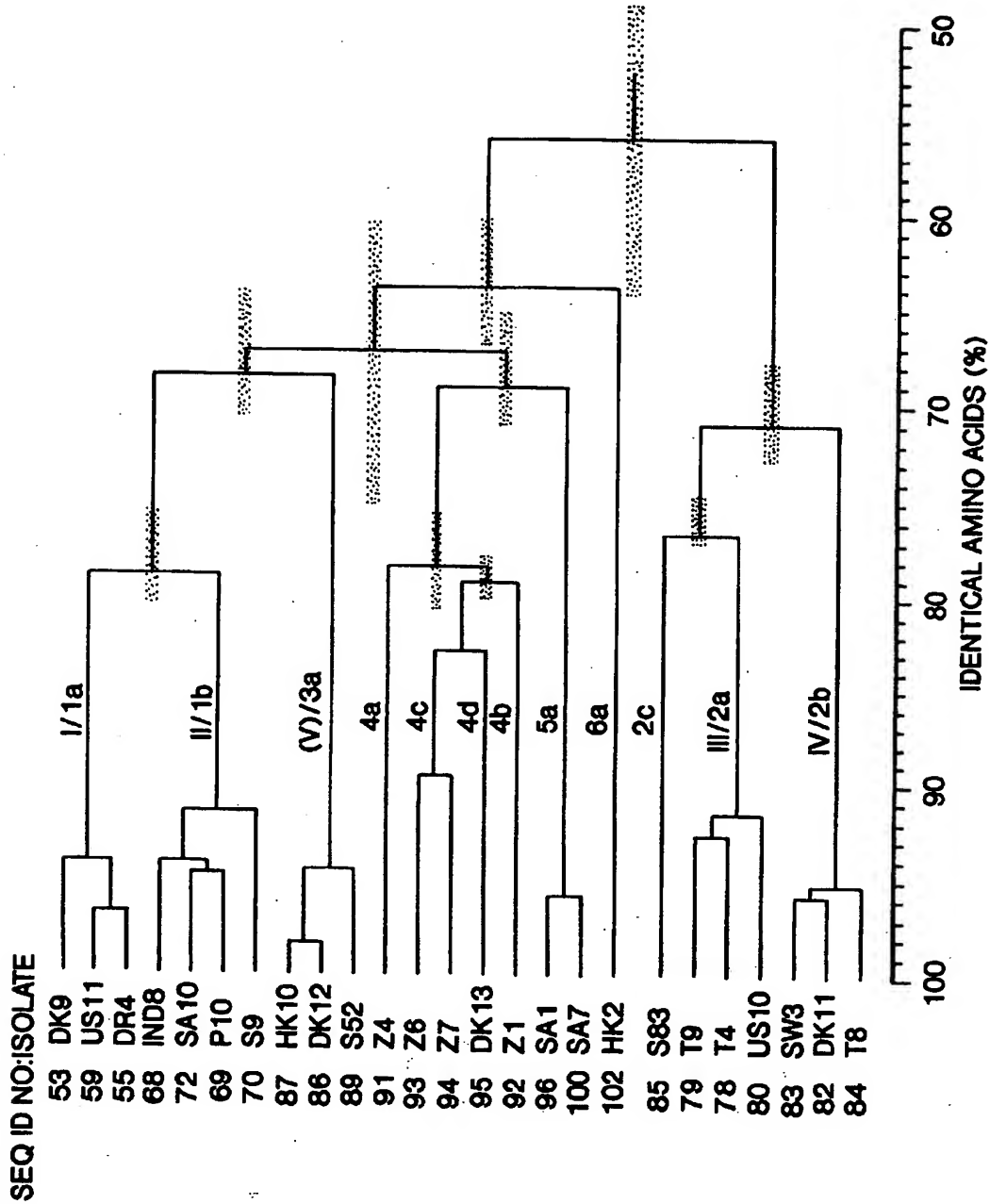
FIGURE 3B

Genotype	SEQ ID NO:	Isolate	290	300	310	320	330	340	350	360	370	380
1V/2b	82	DK11	S-AF1VS-ErhFT-E	I-Q-HIT	L-TLTHLAYAA-V-ELVLEWF-G	WVFL-YFSHQA-A	IAILLVA--DA					
	83	SV3	S-AF1IS-ERHFT-E	I-Q-HIT	L-TLTHLAYAA-V-ELVLEWF-G	WVFL-YFSHQA-A	IAILLVA--DA					
	81	DK8	S-AF1IS-ERHFT-E	I-Q-HIT	L-TLTHLAYAA-V-ELVLEWF-G	WVFL-YFSHQA-A	IAILLVA--DA					
	84	T8	S-AF1IS-ERHFT-E	I-Q-HIT	L-TLTHLAYAA-V-ELVLEWF-G	WVFL-YFSHQA-A	IAILLVA--DA					
2c	85	SV3	A-WWVS-QHNFV-E	I-P-TIT	M-TATHLAYAM-V-EVIDIVS-G	WVFL-YFSHQA-A	IAILLVA--DA					
	78	14	A-MF1VS-QHNFV-E	I-P-TIT	M-TATHLAYAM-V-EVIDIVS-G	WVFL-YFSHQA-A	IAILLVA--DA					
111/2a	80	US10	A-MF1VS-QHNFV-E	I-P-TIT	M-TATHLAYAM-V-EVIDIVS-G	WVFL-YFSHQA-A	IAILLVA--DA					
	79	T9	A-MF1IS-QHNFV-E	I-P-TIT	M-TATHLAYAM-V-EVIDIVS-G	WVFL-YFSHQA-A	IAILLVA--DA					
	77	T2	A-MF1VS-QHNFV-E	I-P-TIT	M-TATHLAYAM-V-EVIDIVS-G	WVFL-YFSHQA-A	IAILLVA--DA					
(V)/3a	86	DK12	G-AFTER-RRHQT-V	I-P-HVS	M-AVGNVAVL-L-QTLFDIA-A	ILAGL-YFSHQA-A	IAILLVA--DA					
	87	HK10	G-AFTER-RRHQT-V	I-P-HVS	M-AVGNVAVL-L-QTLFDIA-A	ILAGL-YFSHQA-A	IAILLVA--DA					
	88	S2	G-AFTER-RRHQT-V	I-P-HVS	M-AVGNVAVL-L-QTLFDIA-A	ILAGL-YFSHQA-A	IAILLVA--DA					
	90	S54	G-AFTER-RRHQT-V	I-P-HVS	M-AVGNVAVL-L-QTLFDIA-A	ILAGL-YFSHQA-A	IAILLVA--DA					
	89	S52	G-AFTER-RRHQT-V	I-P-HVS	M-AVGNVAVL-L-QTLFDIA-A	ILAGL-YFSHQA-A	IAILLVA--DA					
	68	IND8	S-LFTFS-RRHETV-D	I-P-HVS	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	67	IND5	S-LFTFS-RRHETV-D	I-P-HVS	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	73	SH2	S-LFTFS-RRHETV-D	I-P-HVS	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	63	HK3	S-LFTFS-RRHETV-D	I-P-HVS	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	66	HK8	S-LFTFS-RRHETV-D	I-P-HVS	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	71	SA5	S-LFTFS-RRHETV-D	I-P-HVS	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	61	D3	S-LFTFS-RRHETV-E	I-P-HVT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	74	T3	S-LFTFS-RRHETV-D	I-P-HVT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
11/1b	65	HK5	S-LFTFS-RRHETV-D	I-P-HVT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	64	HK4	S-LFTFS-RRHETV-D	I-P-HVS	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	76	US6	S-LFTFS-RRHETV-D	I-P-HVS	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	69	P10	S-LFTFS-RRHETV-D	I-P-HVS	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	72	SA10	S-LFTFS-RRHETV-D	I-P-HVS	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	75	T10	S-LFTFS-RRHETV-D	I-P-HVS	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	62	DK1	S-LFTFS-RRHETV-D	I-P-HVS	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	70	S9	S-LFTIS-RRHETV-D	I-P-HVS	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	60	D1	S-LFTIS-RRHETV-E	I-P-HVT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	52	DK7	G-LFTFS-RRHWT-G	I-P-HIT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	59	US11	G-LFTFS-RRHWT-G	I-P-HIT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	55	DR4	G-LFTFS-RRHWT-D	I-P-HIT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	54	DR1	G-LFTFS-RRHWT-D	I-P-HIT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	53	DK9	G-LFTFS-RRHWT-D	I-P-HIT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	58	SV1	G-LFTFS-RRHWT-D	I-P-HIT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	56	SV14	G-LFTFS-RRHWT-D	I-P-HIT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	57	SV18	G-LFTIS-RRHWT-D	I-P-HIT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	91	Z4	G-MTIF-RRHWT-E	I-T-HIT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
4a	93	Z6	G-MESFQ-RRHWT-D	I-A-HVT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
4c	94	Z7	G-MESFQ-RRHWT-D	I-A-HVT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
4d	95	DK13	G-LFTFQ-RRHWT-D	I-T-HIT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
4b	92	Z1	G-LFGR-RRHWT-D	I-D-HVS	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	98	SA5	G-MFVR-RRHWT-D	I-S-HIT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	100	SA7	G-MFVR-RRHWT-D	I-S-HIT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
5a	97	SA4	G-MFTR-RRHWT-D	I-S-HIT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	96	SA1	G-MFTR-RRHWT-D	I-S-HIT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	99	SA6	G-MFTR-RRHWT-D	I-S-HIT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
	101	SA13	G-MFTYS-RRHWT-D	I-S-HIT	M-TAALWSQIL-L-QAVDNVA-A	VLAGL-YFSHQA-A	IAILLVA--DA					
6a	102	HK2	G-LFTFQ-RRHWT-D	I-T-HVT	M-TAALWSQIL-L-QAVDNVA-A	VLAV-YFSHQA-A	IAILLVA--DA					

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

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Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET



NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

Bukh et al.

Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

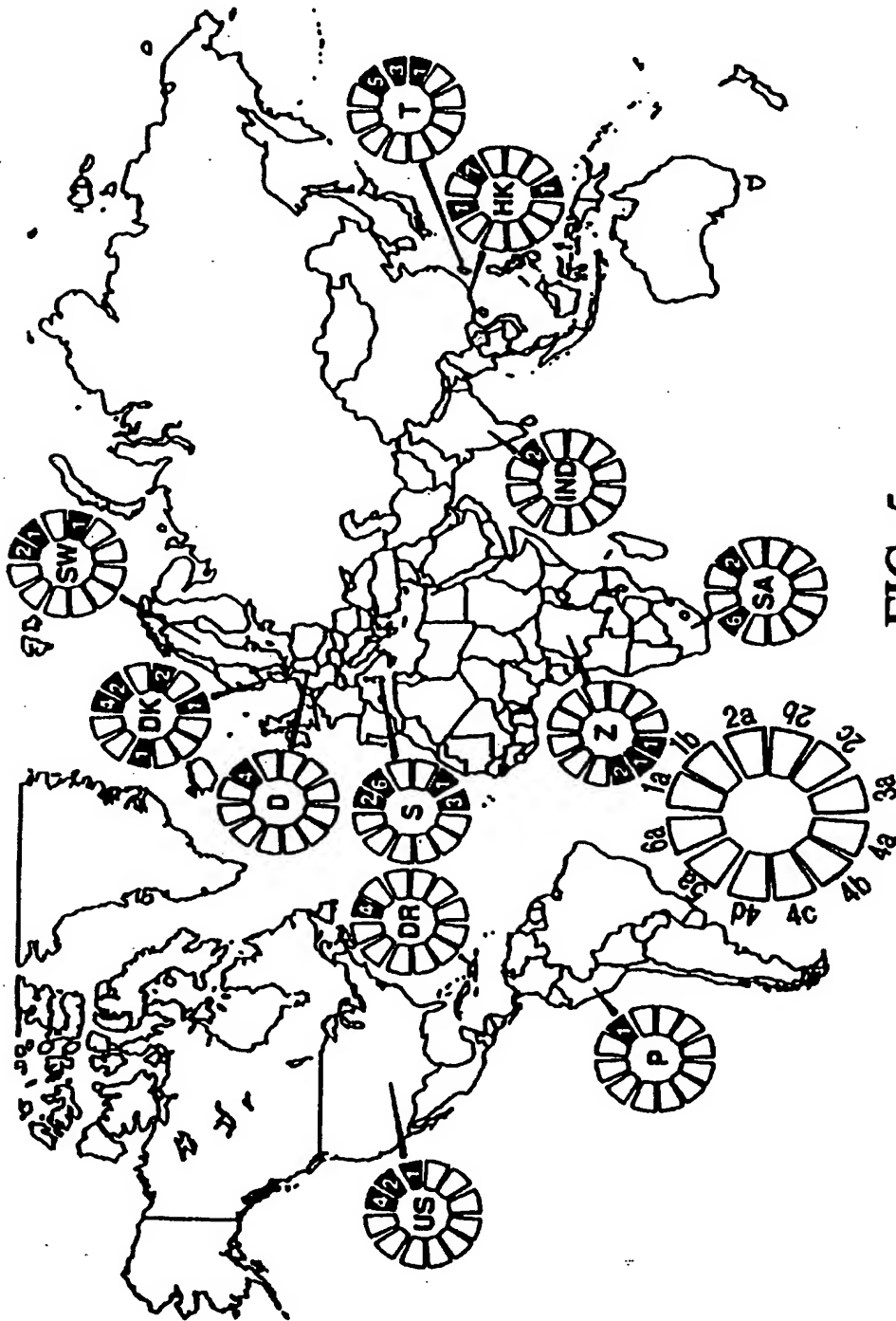


FIGURE 6A-1

SEQ ID NO:	ISOLATE
108	DR4
103	DK7
104	US11
105	S14
106	SW1
107	S18
103-108	consensus
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAACGTAACACCAACCGTCGCCCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAACGTAACACCAACCGTCGCCCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAACGTAACACCAACCGTCGCCCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAACGTAACACCAACCGTCGCCCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAACGTAACACCAACCGTCGCCCCACAGG	
1 ATGAGCACaAATCCTAAACCTCAAAGAAAAAACCAACGTAACACCAACCGTCGCCCCACAGG	
ATGAGCACgAATCCTAAACCTCAAAGAAAAAACCAACGTAACACCAACCGTCGCCCCACAGG	
62 ACGTCAAGTTCCCGGTGGCGGTCAAGTCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG	
62 ACGTCAAGTTCCCGGTGGCGGTCAAGTCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG	
62 ACGTCAAGTTCCCGGTGGCGGTCAAGTCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG	
62 ACGTCAAGTTCCCGGTGGCGGTCAAGTCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG	
62 ACGTCAAGTTCCCGGTGGCGGTCAAGTCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG	
62 ACGTCAAGTTCCCGGTGGCGGTCAAGTCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG	
ACGTcAAGTTCCCGGTGGCGGTCAAGTCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG	
123 CCCTAGATTGGGTGTGCGCGGcGAGGGAAGACTTCCGAGCGGTCCGAACCTCGAGGTAGA	
123 CCCTAGATTGGGTGTGCGCGGcGAGGGAAGACTTCCGAGCGGTCCGAACCTCGAGGTAGA	
123 CCCTAGATTGGGTGTGCGCGGcGAGGGAAGACTTCCGAGCGGTCCGAACCTCGAGGTAGA	
123 CCCTAGATTGGGTGTGCGCGGcGAGGGAAGACTTCCGAGCGGTCCGAACCTCGAGGTAGA	
123 CCCTAGATTGGGTGTGCGCGGcGAGGGAAGACTTCCGAGCGGTCCGAACCTCGAGGTAGA	
123 CCCTAGATTGGGTGTGCGCGGcGAGGGAAGACTTCCGAGCGGTCCGAACCTCGAGGTAGA	
CCCTAGATTGGGTGTGCGCGGcGAGGGAAGACTTCCGAGCGGTCCGAACCTCGAGGTAGA	
108	DR4
103	DK7
104	US11
105	S14
106	SW1
107	S18
103-108	consensus

FIGURE 6A-2

SEQ ID NO:	ISOLATE	
108	DR4	184 CGTCAGCCTATCCCCAAGGCGCTCGGCCCCAGGGCAGGACCTGGGCTCAGCCCCGGGTACC
103	DK7	184 CGTCAGCCTATCCCCAAGGACAGTCGGCCCCAGGGCAGGACCTGGGCTCAGCCCCGGGTACC
104	US11	184 CGTCAGCCTATCCCCAAGGACAGTCGGCCCCAGGGCAGGACCTGGGCTCAGCCCCGGGTACC
105	S14	184 CGTCAGCCTATCCCCAAGGACAGTCGGCCCCAGGGCAGGACCTGGGCTCAGCCCCGGGTATC
106	SW1	184 CGTCAGCCTATCCCCAAGGCGCGTCGGCCCCAGGGCAGGACCTGGGCTCAGCCCCGGGTATC
107	S18	184 CGTCAGCCTATCCCCAAGGCGCGTCGGCCCCAGGGCAGGACCTGGGCTCAGCCCCGGGTACC
103-108	consensus	CGTCAGCCTATCCCCAAGGC - CGTCGGCCCCAGGGCAGGACCTGGGCTCAGCCCCGGGTACC
SEQ ID NO:	ISOLATE	
108	DR4	245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCCCCCGTGG
103	DK7	245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCCCCCGTGG
104	US11	245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCCCCCGTGG
105	S14	245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCCCCCGTGG
106	SW1	245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGaTGGGCGGGATGGCTCCTGTCCCCCGTGG
107	S18	245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGgTGGGCGGGATGGCTCCTGTCCCCCGTGG
103-108	consensus	CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGgTGGGCGGGATGGCTCCTGTCC - CCCCCGTGG
SEQ ID NO:	ISOLATE	
108	DR4	306 CTCTCGGCCCTAGCTGGGGCCCCACAGACCCCGGCGtAGGTCCGCAATTTGGGTAAGGTC
103	DK7	306 CTCTCGGCCCTAGCTGGGGCCCCACAGACCCCGGCGcAGGTCCGCAATTTGGGTAAGGTC
104	US11	306 CTCTCGGCCCTAGCTGGGGCCCCACgGACCCCGGCGTAGGTCCGCAATTTGGGTAAGGTC
105	S14	306 CTCTCGGCCCTAGCTGGGGCCCCACAGACCCCGGCGTAGGTCCGCAATTTGGGTAAGGTC
106	SW1	306 CTCTCGGCCCTAGCTGGGGCCCCACAGACCCCGGCGTAGGTCCGCAATTTGGGTAAGGTC
107	S18	306 CTCcCGGCCCTAGCTGGGGCCCCCTACAGACCCCGGCGTAGGTCCGCAATTTGGGcAAAGTC
103-108	consensus	CTCtCGGCCCTAGCTGGGGCCCCcAcAGACCCCGGCGcTAGGTCCGCAATTTGGGtAAGGTC

FIGURE 6A-3

SEQ ID NO:	ISOLATE	
108	DR4	367 ATCGACACCCTcACGTGCGGCTTCGCCGACCTCATGGGGTACATcCGCTCGTCGGCGCCCC
103	DK7	367 ATCGATACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCC
104	US11	367 ATCGATACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCC
105	S14	367 ATCGATACCCTCAGTGGCGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCC
106	SW1	367 ATCGATACCCTCAGTGGCGCTTCGCCGACCTCATGGGGTACATTCGGCTCGTCGGCGCCCC
107	S18	367 ATCGATACCCTCAGTGGCGCTTCGCCGACCTCATGGGGTACATTCGGCTCGTCGGCGCCCC
103-108	consensus	ATCGATACCCTcACGTGCGGCTTCGCCGACCTCATGGGGTACATaCCGCTCGTCGGCGCCCC
SEQ ID NO:	ISOLATE	
108	DR4	428 CcCTTGgGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGaGTTCTGGAAGACGGCGTGAA
103	DK7	428 CTCTTGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
104	US11	428 CTCTCGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
105	S14	428 CcCTCGGgGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
106	SW1	428 CTCTtGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
107	S18	428 CTCTcGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
103-108	consensus	CtCT - GGaGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGgGTTCTGGAAGACGGCGTGAA
SEQ ID NO:	ISOLATE	
108	DR4	489 CTATGCAACAGGGAAtCTTcCTGGTGTCTTTCTATCTTTCTTTTGGCttTGCTCTCT
103	DK7	489 CTATGCAACAGGGAACCTTCCCTGGTGTCTTTCTATCTTTCTTTTGGCCCTGTCTCT
104	US11	489 CTATGCAACAGGGAACCTTCCCTGGTGTCTTTCTATCTTTCTTTTGGCCCTGTCTCT
105	S14	489 CTATGCAACAGGGAACCTTCCCTGGTGTCTTTCTATCTTTCTTTCTaGCCCTGCTTTCT
106	SW1	489 CTATGCAACAGGGAACCTTCCCTGGTGTCTTTCTATCTTTCTTTCTGCCCCCTGTCTCT
107	S18	489 CTATGCAACAGGGAACCTTCCCTGGTGTCTTTCTATCTTTCTTTCTGCCCCCTGTCTCT
103-108	consensus	CTATGCAACAGGGAACCTTCCCTGGTGTCTTTCTATCTTTCTTCTATCTTTCTGccctTGCTcTCT

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

Bukh et al.

Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

FIGURE 6A-4

<u>SEQ ID NO.</u>	<u>ISOLATE</u>	
108	DR4	550 TGctTGACCGTGCCCGCaTcGGCC
103	DK7	550 TGCCTGACCGTGCCCGCTTCGGCC
104	US11	550 TGCCTGACTGTGCCCCGCTTCAGCC
105	S14	550 TGCCTGACTGTGCCCCGCTTCAGCC
106	SW1	550 TGCCTGACaGTGCCCCGCGTCAGCC
107	S18	550 TGtCTGACTGTGCCCCGCGTCAGct
103-108	consensus	TGccTGACTGTGCCCCGCTTCaGCC

FIGURE 6B-1

SEQ ID NO:	ISOLATE	
119	S9	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
117	IND3	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
118	IND8	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
111	D1	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
112	US6	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
113	P10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
114	DK1	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
115	T10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
116	SW2	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
122	HK4	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
109	SA10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
110	S45	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
123	P8	1 ATGAGCACGACTCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
124	T3	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
120	HK3	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
121	HK5	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
109-124	consensus	ATGAGCACGAaTCCTAAACCTCAAAGAAaAaACCAACGTAACACCAaCCGCGGCCACAGG

SEQ ID NO:	ISOLATE
119	S9
117	IND3
118	IND8
111	D1
112	US6
113	P10
114	DK1
115	T10
116	SW2
122	HK4
1109	SA10
1110	S45
123	P8
124	T3
1120	HK3
121	HK5
109-124	consensus

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

Bukh et al.

Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

FIGURE 6B-3

SEQ. ID NO.	ISOLATE	
119	S9	CCCCAGGTTGGGTGTGCGCGCaACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
117	IND3	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
118	IND8	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
111	D1	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
112	US6	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
113	P10	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
114	DK1	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
115	T10	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
116	SW2	CCCCcGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
122	HK4	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
109	SA10	CCCCAGGTTGGGTGTGCGCGCGACgAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
110	S45	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
123	P8	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
124	T3	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
120	HK3	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTcAGCGGTCCGAACCTCGTGAAGG
121	HK5	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTcAGCGGTCCGAACCTCGTGAAGG
109-124	consensus	CCCCaGGTTGGGTGTGCGCGCGcGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGAAGG

FIGURE 6B-4

SEQ ID NO:	ISOLATE	
119	S9	184 CGACAACCTATCCCCAAGGCTCGCCat CCGAGGGcAGGGCCTGGGCTCAGCCCCGGGTACC
117	IND3	184 CGACAACCTATCCCCAAGGCTCGCCGCCCGAGGGTAGGGCTGGGCTCAGCCCCGGGTACC
118	IND8	184 CGACAACCTATCCCCAAGGCTCGCCGCCCGAGGGTAGGGCTGGGCTCAGCCCCGGGcACC
111	D1	184 CGACAACCTATCCCCAAGGCTCGCCGCCCGAGGGTAGGGCTGGGCTCAGCCCCGGGTACC
112	US6	184 CGACAACCTATCCCCAAGGCTCGCCGCCCGAGGGTAGGGCTGGGCTCAGCCCCGGGTACC
113	P10	184 CGACAACCTATCCCCAAGGCTCGCCGCCCGAGGGTAGGGCTGGGCTCAGCCCCGGGTACC
114	DK1	184 CGACAACCTATCCCCAAGGCTCGCCGCCCGAGGGTAGGGCTGGGCTCAGCCCCGGGTACC
115	T10	184 CGACAACCTATCCCCAAGGCTCGCCGCCCGAGGGTAGGGCTGGGCTCAGCCCCGGGTACC
116	SW2	184 CGACAACCTATCCCCAAGGCTCGCCGCCCGAGGGTAGGGCTGGGCTCAGCCCCGGGTACC
122	HK4	184 CGACAACCTATCCCCAAGGCTCGCCGCCCGAGGGTAGGGCTGGGCTCAGCCCCGGGTACC
109	SA10	184 CGACAACCTATCCCCAAGGCTCGCCGCCCGAGGGTAGGGCTGGGCTCAGCCCCGGGTACC
110	S45	184 CGACAACCTATCCCCAAGGCTCGCCGCCCGAGGGTAGGGCTGGGCTCAGCCCCGGGTACC
123	P8	184 CGACAACCTATCCCCAAGGCTCGCCGCCCGAGGGTAGGGCTGGGCTCAGCCCCGGGTACC
124	T3	184 CGACAACCTATCCCCAAGGCTCGCCGCCCGAGGGTAGGGCTGGGCTCAGCCCCGGGTACC
120	HK3	184 CGACAACCTATCCCCAAGGCTCGCCGCCCGAGGGTAGGGCTGGGCTCAGCCCCGGGTACC
121	HK5	184 CGACAACCTATCCCCAAGGCTCGCCGCCCGAGGGTAGGGCTGGGCTCAGCCCCGGGTACC
109-124	consensus	CGACAaCCTATCCCCCAAGGCTCGCCgGCCGAGGGcAGGgCCTGGGCTCAGCCcGGGtACC

FIGURE 6B-5

SEQ ID NO:	ISOLATE
119	S9
117	IND3
118	IND8
111	D1
112	US6
113	P10
114	DK1
115	T10
116	SW2
122	HK4
109	SA10
110	S45
123	P8
124	T3
120	HK3
121	HK5
109-124	consensus

245 CTTGGCCCCCTCTAcGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGtGG
 245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
 245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
 245 CTTGGCCCCCTCTATGGCAACGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
 245 CTTGGCCCCCTCTATGGCAACGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
 245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
 245 CTTGGCCCCCTCTATGGCAATGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
 245 CTTGGCCCCCTCTATGGCAATGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTCACCCCGtGG
 245 CcTGGCCCCCTCTATGGCAATGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
 245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
 245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
 245 CTTGGCCCCCTCTATGcCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
 245 CTTGGCCCCCTCTATGGCgACGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
 245 CTTGGCCCCCTCTATGGCAACGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
 245 CTTGGCCCCCTCTATGGCAAtGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTCACCCCatGG
 CTTGGCCCCCTCTATGgCaAtGAGGGC-TGGGGTGGGGCaGGATGGCTCCTGTCACCCCgCGG

FIGURE 6B-6

SEQ ID NO:	ISOLATE	
119	S9	306 cTCTCGGCCTAGTTGGGGCCCCAatGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
117	IND3	306 tTCTCGGCCTAGTTGGGGCCCCCAGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
118	IND8	306 CTCTCGGCCTAGTTGGGGCCCCCAGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
111	D1	306 CTCCCGGCCTAGTTGGGGCCCCCAGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
112	US6	306 CTCCCGGCCTAGTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
113	P10	306 CTCTCGGCCTAGTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
114	DK1	306 CTCTCGGCCTAGTTGGGGCCCCCAGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
115	T10	306 CTCcCGGCCTAGTTGGGGCCCCCAGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
116	SW2	306 CTCTCGGCCTAGTTGGGGCCCCCAGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
122	HK4	306 CTCTCGGCCTAGTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGcAATTTGGGTAAGGTC
109	SA10	306 CTCTCGGCCTAGTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
110	S45	306 CTCTCGGCCTAGTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
123	P8	306 CTCCCGGCCTAGTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGCAATTTGGGTAAGGTC
124	T3	306 CTCCCGGCCTAATTTGGGGCCCCCAGACCCCCCGCGTAGGTCGCGTAATcTTGGGTAAGGTC
120	HK3	306 CTCTCGGCCTAATTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGCAATTTGGGTAAGGTC
121	HK5	306 CTCTCGGCCTAgTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
109-124	consensus	cTCTcCGGCCTAgTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGTAATtTGGGTAAGGTC

FIGURE 6B-7

SEQ ID NO:	ISOLATE	
119	S9	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
117	IND3	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
118	IND8	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
111	D1	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
112	US6	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
113	P10	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
114	DK1	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
115	T10	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
116	SW2	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
122	HK4	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
109	SA10	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
110	S45	367 ATCGATACCCCTCACgTGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
123	P8	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGgCC
124	T3	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGGctC
120	HK3	367 ATCGATACCCCTCACGTGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGtGCC
121	HK5	367 ATCGATACCCCTCACGTGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGcGCC
109-124	consensus	ATCGATACCCCTCACaTGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGcGccc

FIGURE 6B-8

SEQ ID NO:	ISOLATE	
119	S9	428 CCCTAGGGGGCGCTGCCAGGGCtCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
117	IND3	428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTcCTGGAGGACGGCGTGAA
118	IND8	428 CCCTAGGGGGTGTCTGCCAGGGCCTGGCGCATGGCGTCCGGTcCTGGAGGACGGCGTGAA
111	D1	428 CCCTAGGGGGTGTCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
112	US6	428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
113	P10	428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
114	DK1	428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
115	T10	428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
116	SW2	428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
122	HK4	428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
109	SA10	428 CtTTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
110	S45	428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
123	P8	428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
124	T3	428 CCtTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
120	HK3	428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
121	HK5	428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
109-124	consensus	CccTAGGGGGcGcTGCCAGgGCcctGGCgCatGGcGTCCGGGtTcTGGAGgACGGCGTGAA

FIGURE 6B-9

SEQ ID NO:	ISOLATE	
119	S9	CTATGCAACAGGGAACcTcCCCGGTGGCTCTTTCTCTATCTTCCTcTgGCTTTGGCTgTCC
117	IND3	CTATGCAACAGGGAACcTgCCCGGTGGCTCTTTCTCTATCTTCCTTTAGCTTTGGCTATCC
118	IND8	CTATGCAACAGGGAACcTgCCCGGTGGCTCTTTCTCTATCTTCCTTTGGCTTTGGCTATCC
111	D1	tTATGCAACAGGGAAtTTGCCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTTTGGCTGTCC
112	US6	CTATGCAACAGGGAACcTgCCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTTTGGCTGTCC
113	P10	CTATGCAACAGGGAAtcTGCCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTTTGGCTGTCC
114	DK1	CTAcGCAACAGGGAATTTGCCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTCTGTgTCC
115	T10	CTATGCAACAGGGAATTTGCCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTCTGGCTGTCT
116	SW2	CTATGCAACAGGGAAtcTGCCCGGTGGCTCcTTTCTCTATCTTCCTCTTGGCTcTGGCTGTCC
122	HK4	CTATGCAACAGGGAATTTGCCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTcTGGCTGTCC
109	SA10	CTATGCAACAGGGAATTTGCCCGGTGGCcCTTTCTCTATCTTCCTCTTGGCTcTGGCTGTCC
110	S45	CTATGCAACAGGGAATCTGCCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTcTGGCTGTCC
123	P8	CTATGCAACAGGGAATCTGCCCTGGTGGCTCTTTCTCTATCTTCCTCTTGGCTTTGGCTGTCT
124	T3	tTAcGCAACAGGGAATTTGCCCTGGTGGCTCTTTCTCTATCTTCCTCTTGGCTTTGGCTGTCC
120	HK3	CTAtGCAACAGGGAATTTAcCCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTTTGGCTGTCC
121	HK5	CTAcGCAACAGGGAAtaTAcCCCGGTGGCTCTTTCTCTATCTTCCTcTTGGCTTTGGCTGTCC
109-124	consensus	cTAtGCAACAGGGAAttTgCCcGGTGGCTcTtTcTCTATCTTCCTctTgGCTtTgCTgTCC

FIGURE 6B-10

SEQ ID NO:	ISOLATE	
119	S9	550 TGTTTGACCATCCAGCTTCCGCT
117	IND3	550 TGTTTGACCATCCAGCTTCCGCT
118	IND8	550 TGTTTGACCGTCCAGCTTCCGCT
111	D1	550 TGTTTGACCATCCAGCTTCCGCT
112	US6	550 TGTTTGACCATCCAGCTTCCGCT
113	P10	550 TGccTGACCATCCAGCGTCCGCT
114	DK1	550 TGttTGACCATCCAGCTTCCGcc
115	T10	550 TGTCTGACCATCCAGCTTCCGCT
116	SW2	550 TGTCTGACCATCCAGCTTCCGCT
122	HK4	550 TGTTTGACCATCCAGCTTCCGCT
109	SA10	550 TGTTTaACCATCCAGCTTCCGCT
110	S45	550 TGctTGACCATCCAGCTTCCGCT
123	P8	550 TGtcTGACCATCCAGCTTCCGCT
124	T3	550 TGCTTGACCATCCAGCTTCCGCT
120	HK3	550 TGCTTGACCACCCCAGCTTCCGCT
121	HK5	550 TGtcTGACCACCCCAGtTCCGCT
109-124	consensus	TGttTgACCatcCCAGctTCCGct

FIGURE 6C-1

SEQ ID NO:	ISOLATE	
119	S9	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
117	IND3	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
118	IND8	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
111	D1	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
112	US6	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
113	P10	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
114	DK1	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
115	T10	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
116	SW2	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
122	HK4	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
109	SA10	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
110	S45	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
123	P8	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
124	T3	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
120	HK3	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
121	HK5	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
108	DR4	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
104	US11	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
105	S14	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
106	SW1	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
107	S18	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
103	DK7	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
103-124	consensus	ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG

FIGURE 6C-2

SEQ ID NO:	ISOLATE	
119	S9	62 ACGTCAAGTTCCCGGGCGGTGGTcCAGATCGTcGGTGGAGTTTACCTGTGCGCGCAGGGG
117	IND3	62 ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTTTACCTGTGCGCGCAGGGG
118	IND8	62 ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTTTACCTGTGCGCGCAGGGG
111	D1	62 ACGTCAAGTTCCCGGGCGGTGGTcCAGATCGTcGGTGGAGTTTACCTGTGCGCGCAGGGG
112	US6	62 ACGTCAAGTTCCCGGGCGGTGGTcCAGATCGTcGGTGGAGTTTACCTGTGCGCGCAGGGG
113	P10	62 ACGTCAAGTTCCCGGGCGGTGGTcCAGATCGTcGGTGGAGTTTACCTGTGCGCGCAGGGG
114	DK1	62 ACGTCAAGTTCCCGGGCGGTGGTcCAGATCGTcGGTGGAGTTTACCTGTGCGCGCAGGGG
115	T10	62 ACGTCAAGTTCCCGGGCGGTGGTcCAGATCGTcGGTGGAGTTTACCTGTGCGCGCAGGGG
116	SW2	62 ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTTTACCTGTGCGCGCAGGGG
122	HK4	62 ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTcGGTGGAGTTTACCTGTGCGCGCAGGGG
109	SA10	62 ACGTCAAGTTCCCGGGCGGTGGTcCAGATCGTcGGTGGAGTTTACCTGTGCGCGCAGGGG
110	S45	62 ACGTCAAGTTCCCGGGCGGTGGTcCAGATCGTcGGTGGAGTTTACCTGTGCGCGCAGGGG
123	P8	62 ACGTCAAGTTCCCGGGCGGTGGTcCAGATCGTcGGTGGAGTTTACCTGTGCGCGCAGGGG
124	T3	62 ACGTCAAGTTCCCGGGCGGTGGTcCAGATCGTcGGTGGAGTTTACCTGTGCGCGCAGGGG
120	HK3	62 ACGTCAAGTTCCCGGGCGGTGGTcCAGATCGTcGGTGGAGTTTACCTGTGCGCGCAGGGG
121	HK5	62 ACGTCAAGTTCCCGGGCGGTGGTcCAGATCGTcGGTGGAGTTTACCTGTGCGCGCAGGGG
108	DR4	62 ACGTCAAGTTCCCGGGCGGTGGTcCAGATCGTcGGTGGAGTTTACCTGTGCGCGCAGGGG
104	US11	62 ACGTCAAGTTCCCGGGCGGTGGCGGTcCAGATCGTcGGTGGAGTTTACTTGTGCGCGCAGGGG
105	S14	62 ACGTCAAGTTCCCGGGCGGTGGCGGTcCAGATCGTcGGTGGAGTTTACTTGTGCGCGCAGGGG
106	SW1	62 ACGTCAAGTTCCCGGGCGGTGGCGGTcCAGATCGTcGGTGGAGTTTACTTGTGCGCGCAGGGG
107	S18	62 ACGTCAAGTTCCCGGGCGGTGGCGGTcCAGATCGTcGGTGGAGTTTACTTGTGCGCGCAGGGG
103	DK7	62 ACGTCAAGTTCCCGGGCGGTGGCGGTcCAGATCGTcGGTGGAGTTTACTTGTGCGCGCAGGGG
103-124	consensus	ACGTCAAGTTCCCGGGCGGTGGTcCAGATCGTcGGTGGAGTTTAcCTGTGCGCGCAGGGG

FIGURE 6C-3

SEQ ID NO:	ISOLATE	
119	S9	123 CCCAGGTTGGGTGTGCGCGCaACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
117	IND3	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
118	IND8	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
111	D1	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
112	US6	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
113	P10	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
114	DK1	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
115	T10	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
116	SW2	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
122	HK4	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
109	SA10	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
110	S45	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
123	P8	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
124	T3	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
120	HK3	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
121	HK5	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
108	DR4	123 CCTAGATTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGAGGTTAGA
104	US11	123 CCTAGATTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGAGGTTAGA
105	S14	123 CCTAGATTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGAGGTTAGA
106	SW1	123 CCTAGATTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGAGGTTAGA
107	S18	123 CCTAGATTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGAGGTTAGA
103	DK7	123 CCTAGATTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGAGGTTAGA
103-124	consensus	CCCcAGTTGGGTGTGCGCGCGaCtAGGAAGACTTcGAGCGgTcgCAACCTCGtGGaaGg

FIGURE 6C-4

SEQ ID NO:	ISOLATE	
119	S9	184 CGACAACCTATCCCCAAGGTCGCatCCCCAGGGcAGGGCCTGGGCTCAGCCCGGGTACC
117	IND3	184 CGACAACCTATCCCCAAGGTCGCGGCCCCGAGGTAGGGCTGGGCTCAGCCCGGGTACC
118	IND8	184 CGACAACCTATCCCCAAGGTCGCGGCCCCGAGGTAGGGCTGGGCTCAGCCCGGGcACC
111	D1	184 CGACAACCTATCCCCAAGGTCGCGGCCCCGAGGTAGGGCTGGGCTCAGCCCGGGTACC
112	US6	184 CGACAACCTATCCCCAAGGTCGCGGCCCCGAGGTAGGGCTGGGCTCAGCCCGGGTACC
113	P10	184 CGACAACCTATCCCCAAGGTCGCGGCCCCGAGGTAGGGCTGGGCTCAGCCCGGGTACC
114	DK1	184 CGACAACCTATCCCCAAGGTCGCGGCCCCGAGGTAGGGCTGGGCTCAGCCCGGGTACC
115	T10	184 CGACAACCTATCCCCAAGGTCGCGGCCCCGAGGTAGGGCTGGGCTCAGCCCGGGTACC
116	SW2	184 CGACAACCTATCCCCAAGGTCGCGGCCCCGAGGTAGGGCTGGGCTCAGCCCGGGTACC
122	HK4	184 CGACAACCTATCCCCAAGGTCGCGGCCCCGAGGTAGGGCTGGGCTCAGCCCGGGTACC
109	SA10	184 CGACAACCTATCCCCAAGGTCGCGGCCCCGAGGTAGGGCTGGGCTCAGCCCGGGTACC
110	S45	184 CGACAACCTATCCCCAAGGTCGCGGCCCCGAGGTAGGGCTGGGCTCAGCCCGGGcAtC
123	P8	184 CGACAACCTATCCCCAAGGTCGCGGCCCCGAGGTAGGGCTGGGCTCAGCCCGGGCACC
124	T3	184 CGACAACCTATCCCCAAGGTCGCGGCCCCGAGGTAGGGCTGGGCTCAGCCCGGGTACC
120	HK3	184 CGACAACCTATCCCCAAGGTCGCGGCCCCGAGGTAGGGCTGGGCTCAGCCCGGGTATC
121	HK5	184 CGACAACCTATCCCCAAGGTCGCGGCCCCGAGGTAGGGCTGGGCTCAGCCCGGGTATC
108	DR4	184 CGTcAGCCTATCCCCAAGGcGCGTcGGCCCCGAGGGcAGGAcCTGGGCTCAGCCCGGGTACC
104	US11	184 CGTcAGCCTATCCCCAAGGcGCGTcGGCCCCGAGGGcAGGAcCTGGGCTCAGCCCGGGTACC
105	S14	184 CGTcAGCCTATCCCCAAGGcGCGTcGGCCCCGAGGGcAGGAcCTGGGCTCAGCCCGGGTATC
106	SW1	184 CGTcAGCCTATCCCCAAGGcGCGTcGGCCCCGAGGGcAGGAcCTGGGCTCAGCCCGGGTATC
107	S18	184 CGTcAGCCTATCCCCAAGGcGCGTcGGCCCCGAGGGcAGGAcCTGGGCTCAGCCCGGGTACC
103	DK7	184 CGTcAGCCTATCCCCAAGGcGCGTcGGCCCCGAGGGcAGGAcCTGGGCTCAGCCCGGGTACC
103-124	consensus	CGaCAaCCTATCCCCAAGGcTcGcCgGCCCCGAGGGcAGGgCCTGGGCTCAGCCcGGGtAcC

FIGURE 6C-5

SEQ ID NO:	ISOLATE	
119	S9	245 CTTGGCCCCCTCTA
117	IND3	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
118	IND8	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
111	D1	245 CTTGGCCCCCTCTATGGCAACGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
112	US6	245 CTTGGCCCCCTCTATGGCAACGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
113	P10	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
114	DK1	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
115	T10	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
116	SW2	245 CcTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
122	HK4	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
109	SA10	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
110	S45	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
123	P8	245 CTTGGCCCCCTCTATGcCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
124	T3	245 CTTGGCCCCCTCTATGGCGACGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
120	HK3	245 CTTGGCCCCCTCTATGGCAACGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
121	HK5	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
108	DR4	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
104	US11	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
105	S14	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
106	SW1	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
107	S18	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
103	DK7	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
103-124	consensus	CtTGGCCCCCTCTATgCaAtGAGGGCcttgGgTGGGCaGgATGGCTCCTGTCaCCCCgtGG

FIGURE 6C-6

SEQ ID NO:	ISOLATE	
119	S9	306 cTCTCGGCCTAGTTGGGGCCCCAaTGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
117	IND3	306 tTCTCGGCCTAGTTGGGGCCCCACAGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
118	IND8	306 CTCTCGGCCTAGTTGGGGCCCCACAGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
111	D1	306 CTCCCGGCCTAGTTGGGGCCCCACcGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
112	US6	306 CTCCCGGCCTAGTTGGGGCCCCACGGAACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
113	P10	306 CTCTCGGCCTAGTTGGGGCCCCACGGAACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
114	DK1	306 CTCTCGGCCTAGTTGGGGCCCCAaCGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
115	T10	306 CTCcCGGCCTAGTTGGGGCCCCACaGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
116	SW2	306 CTCTCGGCCTAGTTGGGGCCCCACtGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
122	HK4	306 CTCTCGGCCTAGTTGGGGCCCCACGGAACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
109	SA10	306 CTCTCGGCCTAGTTGGGGCCCCACGGAACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
110	S45	306 CTCCCGGCCTAGTTGGGGCCCCACGGAACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
123	P8	306 CTCCCGGCCTAGTTGGGGCCCCACGGAACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
124	T3	306 CTCCCGGCCTAATTGGGGCCCCACaGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
120	HK3	306 CTCTCGGCCTAATTGGGGCCCCACGGAACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
121	HK5	306 CTCTCGGCCTAGTTGGGGCCCCACGGAACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
108	DR4	306 CTCTCGGCCTAGTGGGGCCCCACaGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
104	US11	306 CTCTCGGCCTAGTGGGGCCCCACgGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
105	S14	306 CTCTCGGCCTAGTGGGGCCCCACAGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
106	SW1	306 CTCTCGGCCTAGTGGGGCCCCTACAGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
107	S18	306 CTCcCGGCCTAGTGGGGCCCCTACAGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
103	DK7	306 CTCTCGGCCTAGTGGGGCCCCcACAGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
103-124	consensus	cTCTCGGCCTAgTGGGGCCCCAc - GACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC

FIGURE 6C-7

SEQ ID NO:	ISOLATE	
119	S9	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
117	IND3	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
118	IND8	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
111	D1	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
112	US6	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
113	P10	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
114	DK1	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
115	T10	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
116	SW2	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
122	HK4	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
109	SA10	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
110	S45	367 ATCGATACCCCTCACgTGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
123	P8	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGGCC
124	T3	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGGtC
120	HK3	367 ATCGATACCCCTCACGTGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGtGGCC
121	HK5	367 ATCGATACCCCTCACGTGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
108	DR4	367 ATCGAcACCCCTCACGTGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
104	US11	367 ATCGATACCCCTtACGTGGGCTTtGCCGACCTCATGCGGTACATACCGCTCGTCGGCGCCC
105	S14	367 ATCGATACCCCTCACGTGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
106	SW1	367 ATCGATACCCCTCACGTGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
107	S18	367 ATCGATACCCCTCACGTGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
103	DK7	367 ATCGATACCCCTtACGTGGGCTTtGCCGACCTCATGCGGTACATaCCGCTCGTCGGCGCCC
103-124	consensus	ATCGATACCCCTcACaTGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGcGccc

FIGURE 6C-8

SEQ ID NO:	ISOLATE	
119	S9	428 CCCTAGGGGGCGCTGCCAGGGCtCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
117	IND3	428 CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
118	IND8	428 CCCTAGGGGGTGTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
111	D1	428 CCCTAGGGGGTGTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
112	US6	428 CCCTAGGGGGCGCTGCCAGGGCctTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
113	P10	428 CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
114	DK1	428 CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
115	T10	428 CCCTAGGGGGCGCTGCCAGGGctCTGGCaCATGGtGTCCGGGTtCTGGAGGACGGCGTGAA
116	SW2	428 CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
122	HK4	428 CCTTAGGGGGCGtTGCCAGAGCCCTGGCaCATGGtGTCCGGGTtCTGGAGGACGGCGTGAA
109	SA10	428 CtTTAGGGGGCGCTGCCAGAGCCCTTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
110	S45	428 CCCTAGGGGGCGCTGCCAGAGCCCTTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
123	P8	428 CCCTAGGGGGCGTTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
124	T3	428 CctTAGGGGGCGTTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
120	HK3	428 CCCTAGGGGGCGTTGCCAGAGCCtTGGCaCATGGtGTCCGGGTtCTGGAGGACGGCGTGAA
121	HK5	428 CCCTAGGGGGCGTTGCCAGAGCCCTGGCaCATGGtGTCCGGGTtCTGGAGGACGGCGTGAA
108	DR4	428 CCCTtGGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGaGTTCTGGAAGACGGCGTGAA
104	US11	428 CtCTCGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAAGACGGCGTGAA
105	S14	428 CcCTCGGgGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAAGACGGCGTGAA
106	SW1	428 CTCTtGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAAGACGGCGTGAA
107	S18	428 CTCTcGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAAGACGGCGTGAA
103	DK7	428 CTCTtGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAAGACGGCGTGAA
103-124	consensus	CccTaGGgGGcGcTGCCAGgGCcctGGCgCaTGGcGTCCGgGTtctTGGAgGACGGCGTGAA

FIGURE 6C-9

SEQ ID NO:	ISOLATE	
119	S9	CTATGCAACAGGGAACcTCCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
117	IND3	CTATGCAACAGGGAACcTCCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
118	IND8	CTATGCAACAGGGAACcTCCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
111	D1	tTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
112	US6	CTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
113	P10	CTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
114	DK1	CTAcGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
115	T10	CTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
116	SW2	CTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
122	HK4	CTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
109	SA10	CTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
110	S45	CTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
123	P8	CTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
124	T3	tTAcGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
120	HK3	CTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
121	HK5	CTAcGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
108	DR4	CTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
104	US11	CTATGCAACAGGGAACcTTCCCTGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
105	S14	CTATGCAACAGGGAACcTTCCCTGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
106	SW1	CTATGCAACAGGGAACcTTCCCTGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
107	S18	CTATGCAACAGGGAACcTTCCCTGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
103	DK7	CTATGCAACAGGGAACcTTCCCTGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
103-124	consensus	cTAtGCAACAGGGAAtcTgCCcGGTTGctCtTtTcTcTATcTTCCTctTgGcttTgctTgTCC

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

FIGURE 6C-10

SEQ ID NO:	ISOLATE	
119	S9	550 TGTTTGACCATCCAGCTTCCGCT
117	IND3	550 TGTTTGACCATCCAGCTTCCGCT
118	IND8	550 TGTTTGACCATCCAGCTTCCGCT
111	D1	550 TGTTTGACCATCCAGCTTCCGCT
112	US6	550 TGTTTGACCATCCAGCTTCCGCT
113	P10	550 TGcctGACCATCCAGCgTCCGCT
114	DK1	550 TGttTGACCATCCAGCTTCCGCC
115	T10	550 TGCTTGACCATCCAGCTTCCGCT
116	SW2	550 TGCTTGACCATCCAGCTTCCGCT
122	HK4	550 TGTTTGACCATCCAGCTTCCGCT
109	SA10	550 TGTTTaACCATCCAGCTTCCGCT
110	S45	550 TGcTTGACCATCCAGCTTCCGCT
123	P8	550 TGtctGACCATCCAGCTTCCGCT
124	T3	550 TGCTTGACCATCCAGCTTCCGCT
120	HK3	550 TGCTTGACCATCCAGCTTCCGCT
121	HK5	550 TGtcTGACCATCCAGCTTCCGCT
108	DR4	550 TGCTTGACCGTGCCCGCaTcgGCC
104	US11	550 TGCCTGACTGTGCCCGCTTCAGCC
105	S14	550 TGCCTGACTGTGCCCGCTTCAGCC
106	SW1	550 TGCCTGACaGTGCCCGCGTCAGCC
107	S18	550 TGtCTGACTGTGCCCGCGTCAGCT
103	DK7	550 TGcCTGACcGTGCCCGGCTTCgGCC
103-124	consensus	TGttTgACcatcCCaGctTcCGct

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

Bukh et al.

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REPLACEMENT SHEET

FIGURE 6D-1

SEQ ID NO:	ISOLATE	
128	T2	1 ATGAGCACAATTCCTAAACCTCAAGAAAAACCAAGAAACACACACCGTCGCCCAaG
125	T4	1 ATGAGCACAATTCCTAAACCTCAAGAAAAACCAAGAAACACACACCGTCGCCCAaG
126	US10	1 ATGAGCACAATTCCTAAACCTCAAGAAAAACCAAGAAACACACACCGTCGCCCAaG
127	T9	1 ATGAGCACAATTCCTAAACCTCAAGAAAAACCAAGAAACACACACCGTCGCCCAaG
125-128	consensus	ATGAGCACAATTCCTAAACCTCAAGAAAAACCAAGAAACACACACCGTCGCCCAaG
128	T2	62 ACGTTAAGTTCCGGGGCGGGCCAGATCGTTGGCGGAGTATACCTTGCTGCCGCGCAGGGG
125	T4	62 ACGTTAAGTTCCGGGGCGGGCCAGATCGTTGGCGGAGTATACCTTGCTGCCGCGCAGGGG
126	US10	62 ACGTTAAGTTCCGGGGCGGGCCAGATCGTTGGCGGAGTATACCTTGCTGCCGCGCAGGGG
127	T9	62 ACGTTAAGTTCCGGGGCGGGCCAGATCGTTGGCGGAGTATACCTTGCTGCCGCGCAGGGG
125-128	consensus	ACGTTAAGTTCCGGGGCGGGCCAGATCGTTGGCGGAGTATACCTTGCTGCCGCGCAGGGG
128	T2	123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGGAGCGGTCCCAGCCCTCGTGGaAGG
125	T4	123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGGAGCGGTCCCAGCCCTCGTGGaAGG
126	US10	123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGGAGCGGTCCCAGCCCTCGTGGaAGG
127	T9	123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGGAGCGGTCCCAGCCCTCGTGGaAGG
125-128	consensus	CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGGAGCGGTCCCAGCCCTCGTGGaAGG
128	T2	184 CGCCAGCCCCATCCCTAAAGATCGGCGCTCCACTGGCAAGTCTCTGGGGAaAACCCAGGATaCC
125	T4	184 CGCCAGCCCCATCCCTAAAGATCGGCGCTCCACTGGCAAGTCTCTGGGGAaAACCCAGGATaCC
126	US10	184 CGCCAGCCCCATCCCTAAAGATCGGCGCTCCACTGGCAAGTCTCTGGGGAaAACCCAGGATaCC
127	T9	184 CGCCAGCCCCATCCCTAAAGATCGGCGCTCCACTGGCAAGTCTCTGGGGAaAACCCAGGATaCC
125-128	consensus	CGCCAGCCCCATCCCTAAAGATCGGCGCTCCACTGGCAAGTCTCTGGGGAaAACCCAGGATaCC

FIGURE 6D-2

SEQ ID NO:	ISOLATE	
128	T2	245 CCTGGCCCCCTGTATGGGAATGAGGGCTTCGGCTGGGCAGGATGGCTCCTGTCTCCCCCGAGG
125	T4	245 CCTGGCCCCCTGTATGGGAATGAGGGCTTCGGCTGGGCAGGATGGCTCCTGTCTCCCCCGAGG
126	US10	245 CTTGGCCCCCTATATGGGAATGAGGGCTTCGGCTGGGCAGGATGGCTCCTGTCTCCCCCGAGG
127	T9	245 CcTGGCCCTCTATATGGGAATGAGGGCTTCGGCTGGGCAGGATGGCTCCTGTCTCCCCCGAGG
125-128	consensus	CcTGGCCcCT-TATGGGAATGAGGGaCTCGGCTGGGCaGGATGGCTCCTGTCTCCCCCGAGG
SEQ ID NO:	ISOLATE	
128	T2	306 TTCTCGTCCCTCTTGGGGCCCCCAATGACCCCCCGGCATAGGTTCGCGCAATGTGGGTAAaGTC
125	T4	306 TTCCCGTCCCTCcTGGGGCCCCCAATGACCCCCCGGCATAGGTTCGCGCAACGTGGGTAAaGTC
126	US10	306 TTCCCGTCCCTCTTGGGGCCCCCAcTGATCCCCCGGCATAGGTTCGCGCAACGTGGGTAAaGTC
127	T9	306 TTCCCGTCCCTCTTGGGGCCCCCAgTGAcCCCCCGGCATAGGTTCGCGCAACGTGGGTAAaGTC
125-128	consensus	TTCCcCGTCCCTCTTGGGGCCCCCAaTGAcCCCCCGGCATAGGTTCGCGCAAcGTGGGTAAaGTC
SEQ ID NO:	ISOLATE	
128	T2	367 ATCGATAACCCCTAACGTGCGGCTTTGCCGACCTTCATGGGGTACaTCCCCGTCGTAGGGCGcCC
125	T4	367 ATCGATAACCCCTAACGTGCaGcCTTGCCGACCTTCATGGGGTACgTCCCCGTCGTAGGGCGgCC
126	US10	367 ATCGATAACCCCTAACGTGCGGCTTTGCCGACCTTCATGGGgaTACATCCCCGTCGTgGGCGctC
127	T9	367 ATCGATAACCCCTAACGTGCGGCTTTGCCGACCTTCATGGGgTACATCCCCGTCGTaGGCGCCcC
125-128	consensus	ATCGATAACCCCTAACGTGCGGCTTTGCCGACCTTCATGGGgTACaTCCCCGTCGTaGGCGccC
SEQ ID NO:	ISOLATE	
128	T2	428 CGcTtGGTGGTGTGCCAGAGCTCTtGCCGATGGCGTCAGAGTCCTGGAGGACGgaGTTAA
125	T4	428 CGtTgGGTGGCGTGCcCAGAGCTCTCGCGCATGGCGTCAGAGTCCTGGAGGACCGGGTTAA
126	US10	428 CGCTTGGTGGCGTGCcCAGAGCTCTCGCGCATGGCGTCAGgGTCTCTGGAGGACCGGGTTAA
127	T9	428 CGCTTGGTGGCGTtGCCAGAGCTCTCGCGCaCGCGTCAGAGaGTCTCTGGAGGACCGGGTTAA
125-128	consensus	CGcTtGGTGGcGTcGCCAGAGCTCTcGCCGCaTGGCGTCAGAGaGTCTCTGGAGGACGGgGTTAA

FIGURE 6D-3

SEQ ID NO:	ISOLATE	
128	T2	489 TTATGCAACAGGtAACTTACCCGGTTGCTCCTTTTCTATcTTCTTGTaGCCCtgCTGTCC
125	T4	489 TTATGCAACAGGAACTTACCTGGTTGCTCCTTTTCTATcTTCTTGTGCCCCtACTGTCC
126	US10	489 TTATGCAACAGGAACTTACCCGGTTGCTCCTTTTCTATcTTCTTGTGCCCCtACTGTCC
127	T9	489 TTATGCAACAGGAAcTACcTGGTTGCTcTTTTCTATcTTCTTGTGCCCCtACTGTCC
125-128	consensus	TTATGCAACAGGgAAcTACc - GGTtGCTCcTTTTCTATcTTCTTGTgGCCCCTaCTGTCC
SEQ ID NO:	ISOLATE	
128	T2	550 TGCATCAcAtATTCCgGtTtCaGCT
125	T4	550 TGCATCACCAATTCCAGTCTCcGCT
126	US10	550 TGCATCACCAATTCCAGTCTCTGCT
127	T9	550 TGCATCACCAcTCCGgcCTCTGCT
125-128	consensus	TGCATCACcAtTCC-GtcTctGCT

FIGURE 6E-1

SEQ ID NO:	ISOLATE	
131	DK11	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAGAAATACAAACCGCGCCACAGG
132	SW3	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAGAAATACAAACCGCGCCACAGG
133	DK8	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAGAAATACAAACCGCGCCACAGG
129	T8	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAGAAATACAAACCGCGCCACAGG
130	US1	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAGAAATACAAACCGCGCCACAGG
129-133	consensus	ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAGAAATACAAACCGCGCCACAGG
SEQ ID NO:	ISOLATE	
131	DK11	62 ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
132	SW3	62 ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
133	DK8	62 ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
129	T8	62 ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
130	US1	62 ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
129-133	consensus	ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
SEQ ID NO:	ISOLATE	
131	DK11	123 CCCAGGTTGGTGTGCGCaCGACAAGGAAGACTTCGAGCGATCCCAGCGCGTGGGAGA
132	SW3	123 CCCAGGTTGGTGTGCGCGCGACAAGGAAGACTTCGAGCGATCCCAGCGCGTGGGAGA
133	DK8	123 CCCAGGTTGGTGTGCGCGCGACAAGGAAGCTTCGAGCGATCCCAGCGCGTGGGAGg
129	T8	123 CCCTAGTTGGTGTGCGCGCGACAAGGAAGACTTCGAGCGATCCCAGCGCGTGGGAGA
130	US1	123 CCCAGGTTGGTGTGCGCGCGACAAGGAAGACTTCGAGCGATCCCAGCGCGTGGGAGA
129-133	consensus	CCCcAGGTTGGTGTGCGGcCGACAAGGAAGaCTTCGAGCGATCCCAGCGCGTGGGAGa

FIGURE 6E-2

SEQ ID NO:	ISOLATE	
131	DK11	184 CGCCAGCCCATCCGAAAGATCGGCGCTCCACCGCAAGcCCTGGGAAAGCCAGGATATC
132	SW3	184 CGCCAGCCCATCCGAAAGATCGGCGCTCCACCGCAAGTCTTGGGAAAGCCAGGATATC
133	DK8	184 CGCCAGCCCATCCGAAAGATCGGCGCTCCACCGCAAGTCTTGGGAAAGCCgGGATATC
129	T8	184 CGCCAGCCCATCCGAAAGATCGGCGCTCCACCGCAAGTCTTGGGAAAGCCAGGATATC
130	US1	184 CGCCAGCCCATCCGAAAGATCGGCGCTCCACCGCAAGTCTTGGGAAAGCCAGGATATC
129-133	consensus	CGCCAGCCCATCCGAAAGATCGGCGCTCCACCGCAAGTCTTGGGAAAGCCAGGATATC
SEQ ID NO:	ISOLATE	
131	DK11	245 CTTGGCCCCGTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTGGCTCCTGTCCCCCGCGG
132	SW3	245 CTTGGCCCCGTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTGGCTCCTGTCCCCCGCGG
133	DK8	245 CTTGGCCCCGTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTGGCTCCTGTCCCCCGCGG
129	T8	245 CTTGGCCTCTtTACGGAACGAGGGCTGCGGtTGGGCAGGTGGCTCCTGTCCCCCGCGG
130	US1	245 CTTGGCCTCTgTACGGAACGAGGGCTGCGGcTGGGCAGGTGGCTCCTGTCCCCCGCGG
129-133	consensus	CTTGGCCCCGTGTATGGAAACGAGGGCTGCGGcTGGGCAGGTGGCTCCTGTCCCCCGCGG
SEQ ID NO:	ISOLATE	
131	DK11	306 GTCTCATCCTAATTTGGGGCCCCACTGACCCCCGGCATAaATCACGCAATTTGGtAAAGTC
132	SW3	306 GTCTCATCCTAATTTGGGGCCCCACTGACCCCCGGCATAATTCAGCAATTTGGGCAAGTC
133	DK8	306 GTCTCGTCTACTTTGGGGCCCCACTGACCCCCGGCATAATTCAGCAATTTGGGCAAGTC
129	T8	306 GTCTCGTCTACTTTGGGGCCCCACTGACCCCCGGCATAATTCAGTAATTTGGGCAgAGTC
130	US1	306 GTCTCGTCTACTTTGGGGCCCCACTGACCCCCGGCACAAGATCACGTAACTTTGGCAagGTC
129-133	consensus	GTCTCgtCTCTACTTTGGGGCCCCACTGACCCCCGGCAtAgATCACGCAATTTGGGCAaaGTC

FIGURE 6E-3

SEQ ID NO:	ISOLATE	
131	DK11	367 ATCGACACCATTAAGTGTGGTTTGGCCGACCTCATGGGTACATCCCTGTGTCGTGGCGCCC
132	SW3	367 ATCGACACCATTAAGTGTGGTTTGGCCGACCTCATGGGTACATCCCTGTGTCGTGGCGCCC
133	DK8	367 ATCGACACCATTAAGTGTGGTTTGGCCGACCTCATGGGTACATCCCTGTGTCGTGGCGCCC
129	T8	367 ATCGATACCATTAACaTGTGGTTTGGCCGACCTCATGGGTACATCCCTGTGTCGTGGCGCCC
130	US1	367 ATCGATACCATTAACgTGTGGTTTGGCCGACCTCATGGGTACATCCCTGTGTCGTGGCGCCC
129-133	consensus	ATCGACACCATTAACgTGTGGTTTGGCCGACCTCATGGGTACATCCCTGTGTCGTGGCGCCC
SEQ ID NO:	ISOLATE	
131	DK11	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCTTGAAGACGGGATAAA
132	SW3	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCTTGAAGACGGGATAAA
133	DK8	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCTTGAAGACGGGATAAA
129	T8	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCTTGAAGACGGGATAAA
130	US1	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCTTGAAGACGGGATAAA
129-133	consensus	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCTTGAAGACGGGATAAA
SEQ ID NO:	ISOLATE	
131	DK11	489 TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTCTATCTTCTTACTTGTCTCTCTGTca
132	SW3	489 TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTCTATCTTCTTACTTGTCTCTCTGTcG
133	DK8	489 TTACGCAACAGGGAATTTGCCTGGTTGCTCTTTTCTATCTTCTTGTCTCTCTGTCTcG
129	T8	489 cTAcGCAACAGGGAATTTGCCTGGTTGCTCTTTTCTATCTTCTTGTCTCTCTGTCTcCa
130	US1	489 tTAcGCAACAGGGAATcTGcCTGGTTGCTCcTTTTCTATCTTCTTaCTTGTCTCTCTGTcG
129-133	consensus	tTAcGCAACAGGGAATcTGcCTGGTTGCTCtTTTTCTATCTTCTTaCTTGTCTCTCTGTcG

FIGURE 6E-4

<u>SEQ ID NO:</u>	<u>ISOLATE</u>
131	DK11
132	SW3
133	DK8
129	T8
130	US1
129-133	consensus

550	TGCTgCACAGTGCCAGTGTCTGCG
550	TGCTtCACAGTGCCAGTGTCTGCG
550	TGCTgCACAGTGCCAGTGTCTGCG
550	TGCTtCACAGTGCCAGTGTCTGCA
550	TGCGcCACgGTGCCgGTGTCTGCA
	TGct - CACaGTGCCaGTGTCTGCG

SEQ ID NO:	ISOLATE
131	DK11
132	SW3
133	DK8
129	T8C
130	US1
125	T4
126	US10
127	T9
128	T2
134	S83
125-134	consensus
131	DK11
132	SW3
133	DK8
129	T8
130	US1
125	T4
126	US10
127	T9
128	T2
134	S83
125-134	consensus

FIGURE 6F-2

SEQ ID NO:	ISOLATE	
131	DK11	123 CCCAGGTTGGTGTGCGCaCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
132	SW3	123 CCCAGGTTGGTGTGCGCGGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
133	DK8	123 CCCAGGTTGGTGTGCGCGGACAAGGAAGTCTTCCGAGCGATCCCAGCCGCGTGGGAGg
129	T8	123 CCctAGGTTGGTGTGCGCGGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
130	US1	123 CCCAGGTTGGTGTGCGCGGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
125	T4	123 CCCAGGTTGGTGTGCGCGGACAAGGAAGACTTCCGAGCGATCCCAGCCACCTGGGAGG
126	US10	123 CCCAGGTTGGTGTGCGCGGACAAGGAAGACTTCCGAGCGGTCCAGGCCACCTGGGAGG
127	T9	123 CCctAGGTTGGTGTGCGCaCGACAAGGAAGACTTCCGAGCGGTCCAGGCCACCTGGGAGG
128	T2	123 CCCcAGGTTGGTGTGCGCGGACAAGGAAGACTTCCGAGCGGTCCAGGCCctCGTGGAAGG
134	S83	123 CCCgAGaTTGGTGTGCGCGGACgAGGAaAaACTTCCGAaCGGTCCCAGGCCaCGTGgGgAGG
125-134	consensus	CCCcAGgTTGGTGTGCGCGCGACaAGGAAGaCTTCCgAGCGaTCCCAGCCgCGTGgGgAGg
131	DK11	184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGcCCTGGGAAAGCCAGGATATC
132	SW3	184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAAGCCAGGATATC
133	DK8	184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAaAaCCgGGATATC
129	T8	184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAaAaCCAGGATATC
130	US1	184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAaAaCCAGGATATC
125	T4	184 CGCCAGCCCCATCCCAAGATCGGCGCTCCACTGGCAAGTCTTGGGAAaAaCCAGGATATC
126	US10	184 CGCCAGCCCCATCCCAAGATCGGCGCcCCACTGGCAAGTCTTGGGAAaAaCCAGGATACC
127	T9	184 CGCCAGCCCCATCCCAAGATCGGCGCTCCACTGGCAAGTCTTGGGAAaAaCCAGGATACC
128	T2	184 CGCCAGCCCCATCCCTAAAGATCGGCGCTCCACTGGCAAGTCTTGGGAAaAaCCAGGATACC
134	S83	184 CGCCAGCCCCATCCCTAAAGATCGGCGCaCCACTGGCAAGTCTTGGGAAAggCCAGGATACC
125-134	consensus	CGCCAGCCCCATCCCGAAAGATCGGCGCTCCAC-GGCAAGTCTTGGGAAaAaCCaGGATATC

FIGURE 6F-3

SEQ ID NO:	ISOLATE
131	DK11
132	SW3
133	DK8
129	T8
130	US1
125	T4
126	US10
127	T9
128	T2
134	S83
125-134	consensus
245	CTTGGCCCCCTGTATGGAACGAGGGCTGCGGCTGGGAGGTTGGCTCCTGTCCCCCCCCCGGG
245	CTTGGCCCCCTGTATGGAACGAGGGCTGCGGCTGGGAGGTTGGCTCCTGTCCCCCCCCCGGG
245	CTTGGCCCCCTGTATGGAACGAGGGCTGCGGCTGGGAGGTTGGCTCCTGTCCCCCCCCCGGG
245	CTTGGCCCTCTTACGGAACGAGGGCTGCGGCTGGGAGGTTGGCTCCTGTCCCCCCCCCGGG
245	CTTGGCCCTCTTACGGAACGAGGGCTGCGGCTGGGAGGTTGGCTCCTGTCCCCCCCCCGGG
245	CcTGGCCCCCTGTATGGAATGAGGACTCGGCTGGGAGGATGGCTCCTGTCCCCCCCCGAGG
245	CtTGGCCCCCTGTATGGAATGAGGACTCGGCTGGGAGGATGGCTCCTGTCCCCCCCCGAGG
245	CCTGGCCCTCTATATGGAATGAGGACTCGGCTGGGAGGATGGCTCCTGTCCCCCCCCGAGG
245	CCTGGCCCCCTGTATGGAATGAGGAGCTCGGCTGGGAGGATGGCTCCTGTCCCCCCCCGAGG
245	CtTGGCCCCCTGTATGGAATGAGGAGCTCGGCTGGGAGGATGGCTCCTGTCCCCCCCCGCGG
	CtTGGCCcCTgTAtGG-AA-GAGGGc--CGGcTGGGCaGGtTGGCTCCTGTCCCCCCCCCGGG
306	GTCTCATCCTAATTGGGGCCCCCACTGACCCCCGGCATAAATCACGCAATTGGGTAAAGTC
306	GTCTCATCCTAATTGGGGCCCCCACTGACCCCCGGCATAGATCACGCAATTGGGGCAAAGTC
306	GTCTCGTCTACTTGGGGCCCCCACTGACCCCCGGCATAGATCACGCAATTGGGGCAAAGTC
306	GTCTCGTCTACTTGGGGCCCCCACTGACCCCCGGCATAGATCACGTAATTGGGGCAAGTC
306	GTCTCGTCTACTTGGGGCCCCCACTGACCCCCGGCACAGATCACGTAATTGGGGCAAGTC
306	TTCCCGTCCCTCcTGGGGCCCCCAaTGACCCCCGGCATAGGTCCGGCAACGTGGGTAAAGTC
306	TTCCCGTCCCTCTTGGGGCCCCCAcTGATCCCCGGCATAGGTCCGGCAACGTGGGTAAAGTC
306	TTCCCGTCCCTCTTGGGGCCCCCAgTGACCCCCGGCATAGGTCCGGCAACGTGGGTAAAGTC
306	TTCTCGTCCCTCTTGGGGCCCCCAaTGACCCCCGGCATAGGTCCGGCAATGTGGGTAAaGTC
306	TTCTCGcCCTTCaTGGGGCCCCCAccGACCCCCGGCATAAaTCGGCGCAActTGGGTAAgGTC
125-134	-TcTcGtCCt-ctTGGGGCCCCCAcTGAcCCCCGGCaTAgATC-CGcAA-tTGGGTAA-GTC
SEQ ID NO:	ISOLATE
131	DK11
132	SW3
133	DK8
129	T8
130	US1
125	T4
126	US10
127	T9
128	T2
134	S83
125-134	consensus

FIGURE 6F-4

SEQ ID NO:	ISOLATE	
131	DK11	367 ATCGACACCATTAACGTGTGGTTTTTGGCGACCTCATGGGGTACATCCCTGTCGTcGGCGCCC
132	SW3	367 ATCGACACCATTAACGTGTGGTTTTTGGCGACCTCATGGGGTACATCCCTGTCGTGGCGCCC
133	DK8	367 ATCGACACCATTAACGTGTGGTTTTTGGCGACCTCATGGGGTACATCCCTGTCGTGGCGCCC
129	T8	367 ATCGATACCATTAACGTGTGGTTTTTGGCGACCTCATGGGGTACATCCCTGTCGTGGCGCCC
130	US1	367 ATCGATACCATTAACGTGTGGTTTTTGGCGACCTCATGGGGTACATCCCTGTCGTGGCGCCC
125	T4	367 ATCGATACCCCTAACGTGCaGcCTTGGCGACCTCATGGGGTACgTCCCCGTCGTaGGCGcC
126	US10	367 ATCGATACCCCTAACGTGCGGCTTTGGCGACCTCATGGGGTACATCCCGTCGTGGCGcC
127	T9	367 ATCGATACCCCTAACGTGCGGCTTTGGCGACCTCATGGGGTACATCCCGTCGTGGCGcC
128	T2	367 ATCGATACCCCTAACGTGCGGCTTTGGCGACCTCATGGGGTACATCCCGTCGTGGCGcC
134	S83	367 ATCGATACCCCTAACGTGCGGCTTTGGCGACCTCATGGGGTACATaCCCCGTCGTtGGCGcC
125-134	consensus	ATCGATACC-T-ACgTG-gGttTTGCCGACCTCAIGGGgTACaTcCC-GTCGTtGGCGccc
SEQ ID NO:	ISOLATE	
131	DK11	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTTAGAGTCCTGGAAGACGGGATAAA
132	SW3	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTTAGAGTCCTGGAAGACGGGATAAA
133	DK8	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTTAGAGTCCTGGAAGACGGGATAAA
129	T8	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTTAGAGTCCTGGAAGACGGGATAAA
130	US1	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTTAGAGTCCTGGAAGACGGGATAAA
125	T4	428 CgLTgGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGaGTCTCTGGAGGACGGGGTTAA
126	US10	428 CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGgGTCTCTGGAGGACGGGGTTAA
127	T9	428 CGCTTGGTGGCGTtGCCAGAGCTCTCGCGCaCGGCGTGAGAGTCCTGGAGGACGGGGTTAA
128	T2	428 CGCTTGGTGGtGTcGCCAGAGCTCTtGCCATGGCGTGAGAGTCCTGGAGGACGGaGTTAA
134	S83	428 CcgTTGGcGGcGTTtGCCAGAGCCcTcGccCATGGgGTGAGgGTTtCTGGAGGACGGgaTaaa
125-134	consensus	CggTtGGaGGcGTcGCCAGAGCtCTgCaCA-GGtGT-AG-GTcCTGGA-GACGGgaTaaa

SEQ ID NO:	ISOLATE
131	DK11
132	SW3
133	DK8
129	T8
130	US1
125	T4
126	US10
127	T9
128	T2
134	S83
125-134	consensus
131	DK11
132	SW3
133	DK8
129	T8
130	US1
125	T4
126	US10
127	T9
128	T2
134	S83
125-134	consensus

FIGURE 6G-1

SEQ ID NO:	ISOLATE	
138	DK12	1 ATGAGCACACTTCCTAAACCTCAAGAAGAAAAACCAAGAAAAACCAATCCGTCGCCCCACAGG
135	HK10	1 ATGAGCACACTTCCTAAACCTCAAGAAGAAAAACCAAGAAAAACCAATCCGTCGCCCCACAGG
136	S52	1 ATGAGCACACTTCCTAAACCTCAAGAAGAAAAACCAAGAAAAACCAATCCGTCGCCCCACAGG
137	S2	1 ATGAGCACACTTCCTAAACCTCAAGAAGAAAAACCAAGAAAAACCAATCCGTCGCCCCACAGG
135-138	consensus	ATGAGCACACTTCCTAAACCTCAAGAAGAAAAACCAAGAAAAACCAATCCGTCGCCCCACAGG
SEQ ID NO:	ISOLATE	
138	DK12	62 ACGTCAAGTTCCCGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTGCCGCGCAGGGG
135	HK10	62 ACGTCAAGTTCCCGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTGCCGCGCAGGGG
136	S52	62 ACGTCAAGTTCCCGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTGCCGCGCAGGGG
137	S2	62 ACGTCAAGTTCCCGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTGCCGCGCAGGGG
135-138	consensus	ACGTCAAGTTCCCGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTGCCGCGCAGGGG
SEQ ID NO:	ISOLATE	
138	DK12	123 CCCACGATTGGGTGTGCGCGGACGCGTAAACTTCTGAACGGTCA CAGCCTCGCGGACGg
135	HK10	123 CCCACGATTGGGTGTGCGCGGACGCGTAAACTTCTGAACGGTCA CAGCCTCGCGGACGg
136	S52	123 CCCACGATTGGGTGTGCGCGGACGCGTAAACTTCTGAACGGTCA CAGCCTCGCGGACGg
137	S2	123 CCCACGATTGGGTGTGCGCGGACGCGTAAACTTCTGAACGGTCA CAGCCTCGCGGACGg
135-138	consensus	CCCACGATTGGGTGTGCGCGGACGCGTAAACTTCTGAACGGTCA CAGCCTCGCGGACG-
SEQ ID NO:	ISOLATE	
138	DK12	184 CGACAGCCTATCCCCAAGGCGGTGGAGCGAAGGCCGGTCTGGGCTCAGCCTGGGTACC
135	HK10	184 CGACAGCCTATCCCCAAGGCGGTGGAGCGAAGGCCGGTCTGGGCTCAGCCTGGGTACC
136	S52	184 CGACAGCCTATCCCCAAGGCGGTGGAGCGAAGGCCGGTCTGGGCTCAGCCTGGGTACC
137	S2	184 CGACAGCCTATCCCCAAGGCGGTGGAGCGAAGGCCGGTCTGGGCTCAGCCTGGGTACC
135-138	consensus	CGACAGCCTATCCCCAAGGCGGTGGAGCGAAGGCCGGTCTGGGCTCAGCCTGGGTACC

FIGURE 6G-2

SEQ ID NO:	ISOLATE	
138	DK12	245 CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGAGGgTGGCTCCTGTCCCCACGCGG
135	HK10	245 CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGAGGgTGGCTCCTGTCCCCACGCGG
136	S52	245 CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGAGGgTGGCTCCTGTCCCCACGCGG
137	S2	245 CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGAGGgTGGCTCCTGTCCCCACGCGG
135-138	consensus	CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGAGGgTGGCTCCTGTCCCCACGCGG
SEQ ID NO:	ISOLATE	
138	DK12	306 CTCCCGTCCATCTTGGGGCCCAACGACCCCCGGCGgaGGTCCCGCAATTGGGTAAGTC
135	HK10	306 CTCCCGTCCATCTTGGGGCCCAACGACCCCCGGCGgaGGTCCCGCAATTGGGTAAGTC
136	S52	306 CTCCCGTCCATCTTGGGGCCCAACGACCCCCGGCGgaGGTCCCGCAATTGGGTAAGTC
137	S2	306 CTCCCGTCCATCTTGGGGCCCAAAAGACCCCCGGCGgaGGTCCCGCAATTGGGTAAGTC
135-138	consensus	CTCCCGTCCATCTTGGGGCCCAACGACCCCCGGCGgaGGTCCCGCAATTGGGTAAGTC
SEQ ID NO:	ISOLATE	
138	DK12	367 ATCGATACCCCTACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
135	HK10	367 ATCGATACCCCTACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
136	S52	367 ATCGATACCCCTACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
137	S2	367 ATCGATACCCCTACGTGCGGcTTGCGCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
135-138	consensus	ATCGATACCCCTACGTGCGGgATTGCGCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
SEQ ID NO:	ISOLATE	
138	DK12	428 CtGTAGGgGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA
135	HK10	428 CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA
136	S52	428 CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA
137	S2	428 CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA
135-138	consensus	CcGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA

FIGURE 6G-3

SEQ ID NO:	ISOLATE	
138	DK12	489 TTTGCAACAGGAACTTGCCCGGTTGCTCCTTTCTATCTTCCTTCTTGCTCTGTTCTCT
135	HK10	489 TTTGCAACAGGAACTTGCCCGGTTGCTCCTTTCTATCTTCCTTCTTGCTCTGTTCTCT
136	S52	489 TTTTGGCAACAGGAACTTGCCCGGTTGCTCCTTTCTATCTTCCTTCTTGCTCTGTTCTCC
137	S2	489 TTTTGGCAACAGGAACTTGCCCGGTTGCTCCTTTCTATCTTCCTTCTTGCTCTGTTCTCT
135-138	consensus	TTT-GCAACAGGAACTTGCCCGGTTGCTCCTTTCTATCTTCCTTCTTGCTCTGTTCTCT
SEQ ID NO:	ISOLATE	
138	DK12	550 TGCCTAATTTCATCCAGCAGCTAGT
135	HK10	550 TGCCTAATTTCATCCAGCAGCTAGT
136	S52	550 TGCTTAGTTTCATCCTGCAGCTAGT
137	S2	550 TGCTTAATTTCATCCAGCAGCTAGT
135-138	consensus	TGCTTAATTTCATCCAGCAGCTAGT

FIGURE 6H-1

SEQ ID NO:	ISOLATE	
145	DK13	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCGCGCGCCCAATGG
143	Z6	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCGCGCGCCCAATGG
144	Z7	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCGCGCGCCCAATGG
140	Z8	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCGCGCGCCCAATGG
139	Z4	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCGCGCGCCCAATGG
142	Z5	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCGCGCGCCCAATGG
141	Z1	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCGCGCGCCCAATGG
139-145	consensus	ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCGCGCGCCCAATGG
SEQ ID NO:	ISOLATE	
145	DK13	62 ACGTTAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTTGTTCGCGCGCAGGGG
143	Z6	62 ACGTTAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTTGTTCGCGCGCAGGGG
144	Z7	62 ACGTTAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTTGTTCGCGCGCAGGGG
140	Z8	62 ACGTTAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTTGTTCGCGCGCAGGGG
139	Z4	62 ACGTTAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTTGTTCGCGCGCAGGGG
142	Z5	62 ACGTTAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTTGTTCGCGCGCAGGGG
141	Z1	62 ACGTTAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTTGTTCGCGCGCAGGGG
139-145	consensus	ACGT-AAAGTTCCCGGGTGGTGGCAGATCGTTGGCGGAGTTTACTTTGTTCGCGCGCAGGGG
SEQ ID NO:	ISOLATE	
145	DK13	123 CCCAGaTTGGGTGTGCGCGGACTAGGAAGACTTCGGAGCGGTGCGCAACCTCGTGGGAGG
143	Z6	123 CCCAGaTTGGGTGTGCGCGGACTAGGAAGACTTCGGAGCGGTGCGCAACCTCGTGGGAGG
144	Z7	123 CCCAGaTTGGGTGTGCGCaCaACTAGGAAGACTTCGGAGCGGTGCGCAACCTCGTGGGAGG
140	Z8	123 CCCAGaTTGGGTGTGCGCGGACTCGGAAGACTTCGGAGCGGTGCGCAACCTCGTGGCAGG
139	Z4	123 CCCAGaTTGGGTGTGCGCGGACTCGGAAGACTTCGGAGCGGTGCGCAACCTCGTGGCAGG
142	Z5	123 CCCAGaTTGGGTGTGCGCGGACTCGGAAGACTTCGGAGCGGTGCGCAACCTCGCGGCGAGG
141	Z1	123 CCCCGGTGGGTGTGCGCGGAGCTCGGAAGACTTCGGAGCGGTGCGCAACCTCGTGGCAGG
139-145	consensus	CCCCaGgTTGGGTGTGCGCGGCGaCTCGGAAGACTTCGGAGCGGTGCGCAACCTCGTGGCAGG

FIGURE 6H-2

SEQ ID NO:	ISOLATE	
145	DK13	
143	Z6	184 CGCAGCCTATCCCCAAGGCGCGcCaActcGAGGGtAGGTCTTGGGCTCAGCCTGGGTATC
144	Z7	184 CGCAGCCTATCCCCAAGGCGCGcCaActcGAGGGtAGGTCTTGGGCTCAGCCCCGGTATC
140	Z8	184 CGTCAGCCTATCCCCAAGGCGCGcCaActcGAGGGtAGGTCTTGGGCTCAGCCCCGGGTACC
139	Z4	184 CGTCaACCTATCCCCAAGGCGCGcCaGAGGGCAGaTCTTGGGCGCAGCCCCGGGTACC
142	Z5	184 CGTCAGCCTATCCCCAAGGCGCGcCGGTCCGAGGGCAGGTCTTGGGCTCAGCCCCGGGTACC
141	Z1	184 CGTCAGCCTATCCCCAAGGCGCGcCGGTCCGAGGGCAGGTCTTGGGCTCAGCCCCGGGTACC
139-145	consensus	CGtCAGCCTATCCCCAAGGCGCGtCggtccGAGGGcAGgTCTTGGGCTCAGCCCCGGGTACC
145	DK13	
143	Z6	245 CtTGGCCcCTTTACGGcCAATGAGGGcTGCGGGTGGCGGGATGGCTCCTGTCACCCCGTGG
144	Z7	245 CATGGCCCTTTTACGGTAATGAGGGTTCGGGTGGCGGGATGGCTCCTGTCACCCCGTGG
140	Z8	245 CATGGCCCTTTTACGGTAACGAGGGTTCGGGTGGCGGGATGGCTCCTGTCACCCCGTGG
139	Z4	245 CATGGCCCTTTTACGGTAATGAaGGCTGcGGGTGGCGAGGTGGCTCCTGTCTCCCCCGCGG
142	Z5	245 CTTGGCCcCTcTATGGCAATGAGGGCTGcGGGTGGCGAGGTGGCTCCTGTCTCCCCCGCGG
141	Z1	245 CTTGGCCcCTTTTACGGCAATGAGGGCTGcGGGTGGCGAGGTGGCTCCTGTCTCCCCCGCGG
139-145	consensus	CtTGGCCcCTtTAcGGcCAAtGAGGcTGcGGGTGGGCaGG-TGGCTCCTGTCTC-CCCCCGcGG
145	DK13	
143	Z6	306 CTCTCGGCGGTCTTGGGGcCCgAATGATCCCCGGCGgAGGTCCCCGCAACTTGGGTAAAGTC
144	Z7	306 CTCTCGACCGTCTTGGGGcCCAAATGATCCCCGGCGAAGGTCCCCGCAACTTGGGTAAAGTC
140	Z8	306 CTCTCGACCGTCTTGGGGcCCAAATGATCCCCGGCGAAGGTCCCCGCAACTTGGGTAAAGTC
139	Z4	306 CTCTCGACCGTCTTGGGGcCCAAATGATCCCCGGCGGAGGTCCGCGCAATTTGGGTAAAGTC
142	Z5	306 CTCTCGGCCCATCTTGGGGcCCAAATGATCCCCGGCGGAGaTCCGCGCAATCTGGGTAAAGTC
141	Z1	306 aTCTCGGCCCATCTTGGGGcCCAAATGATCCCCGGCGGTAGGTCCCGCAATCTGGGTAAAGTC
139-145	consensus	tTcCaGGCCcTCTTGGGGCCcCAATGATCCCCGGCGGTAGGTCCCCGTAAATCTGGGTAAaGTC
145	DK13	
143	Z6	cTCTcGgCCgTCTTGGGGcCCaAATGATCCCCGGCGGAGgTCCcCGcAAAtTGGGTAAAGTC
144	Z7	
140	Z8	
139	Z4	
142	Z5	
141	Z1	
139-145	consensus	

SEQ ID NO:	ISOLATE
145	DK13
143	Z6
144	Z7
140	Z8
139	Z4
142	Z5
141	Z1
139-145	consensus
145	DK13
143	Z6
144	Z7
140	Z8
139	Z4
142	Z5
141	Z1
139-145	consensus
145	DK13
143	Z6
144	Z7
140	Z8
139	Z4
142	Z5
141	Z1
139-145	consensus

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
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FIGURE 6H-4

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
145	DK13	550 TGCCTgACTGTtCCCGctTCGGCC
143	Z6	550 TGCCTaACTGTtCCCaCCTCGGCC
144	Z7	550 TGCCTgACTGTtCCCGCCtCGGCC
140	Z8	550 TGCCTaACcGTcCCAGCGTctGCT
139	Z4	550 TGCCTcACTGTtCCAGCGTCgGCT
142	Z5	550 TGCTTGACAACACCGGCATCcGCT
141	Z1	550 TGCcTGACAACACCaGCATCtGCC
139-145	consensus	TGCcTgACTgttCC-gC-TCgGCC

FIGURE 6I-1

SEQ ID NO:	ISOLATE
153	SA11
152	SA6
146	SA4
147	SA5
148	SA7
149	SA1
150	SA3
151	SA13
146-153	consensus
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCGCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCGCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCGCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCGCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCGCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCGCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCGCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCGCCACAGG	
ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCGCCACAGG	
62 ACGTCAAGTTCGCCGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGG	
62 ACGTCAAGTTCGCCGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGG	
62 ACGTCAAGTTCGCCGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGG	
62 ACGTCAAGTTCGCCGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGG	
62 ACGTCAAGTTCGCCGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGG	
62 ACGTCAAGTTCGCCGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGG	
62 ACGTCAAGTTCGCCGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGG	
ACGTCAAGTTCGCCGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGG	
123 CCCTaGgtTGGGTGTGCGCGCGACTCGGAAGAATTTCaGAACGGTCGCAACCCCGTGGgCGG	
123 CCCTcGtaTGGGTGTGCGCGCGACTCGGAAGAATTTCgGAACGGTCGCAACCCCGTGGaCGG	
123 CCCTAGgtTGGGTGTGCGCGCGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG	
123 CCCTAGaTTGGGTGTGCGCGCGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG	
123 CCCTAGTTGGGTGTGCGCGCGACTCGGAAGAATTTCAGAACGGTCGCAACCCCGTGGGCGG	
123 CCCcAGgtTGGGTGTGCGCGCGACTCGGAAGAATTTCgGAACGGTCGCAACCCCGTGGGCGG	
123 CCCcAGGTTGGGTGTGCGCGCGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGACCGG	
123 CCCcAGGTGGGTGTGCGCGCGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGACCGG	
123 CCCTaGgtTGGGTGTGCGCGCGaACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGACCGG	
CCCTaGgtTGGGTGTGCGCGCGgACTCGGAAGAATTTCaGAACGGTCGCAACCCCGTGGgCGG	
SEQ ID NO:	ISOLATE
153	SA11
152	SA6
146	SA4
147	SA5
148	SA7
149	SA1
150	SA3
151	SA13
146-153	consensus
123 CCCTaGgtTGGGTGTGCGCGCGACTCGGAAGAATTTCaGAACGGTCGCAACCCCGTGGgCGG	
123 CCCTcGtaTGGGTGTGCGCGCGACTCGGAAGAATTTCgGAACGGTCGCAACCCCGTGGaCGG	
123 CCCTAGgtTGGGTGTGCGCGCGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG	
123 CCCTAGaTTGGGTGTGCGCGCGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG	
123 CCCTAGTTGGGTGTGCGCGCGACTCGGAAGAATTTCAGAACGGTCGCAACCCCGTGGGCGG	
123 CCCcAGgtTGGGTGTGCGCGCGACTCGGAAGAATTTCgGAACGGTCGCAACCCCGTGGGCGG	
123 CCCcAGGTTGGGTGTGCGCGCGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGACCGG	
123 CCCcAGGTGGGTGTGCGCGCGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGACCGG	
123 CCCTaGgtTGGGTGTGCGCGCGaACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGACCGG	
CCCTaGgtTGGGTGTGCGCGCGgACTCGGAAGAATTTCaGAACGGTCGCAACCCCGTGGgCGG	

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

Bukh et al.

Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

FIGURE 6I-2

SEQ ID NO:	ISOLATE	
153	SA11	184 CGTCAGCCTATTCCCAAGGCGGCCCAACCCaCGGGcCGGTCTTGGGGTCAACCCCGGGTACC
152	SA6	184 CGTCAGCCTATTCCCAAGGCGGCCCAATCCgCGGGtCGGTCTTGGGGTCAACCCCGGGTACC
146	SA4	184 CGCCAGCCTATTCCCAAGGCGGCCCAACCCaCGGGCCGGTCTTGGGGTCAACCCCGGGTACC
147	SA5	184 CGCCAGCCTATTCCCAAGGCGGCCCAACCCaCGGGCCGGTCTTGGGGTCAACCCCGGGTACC
148	SA7	184 CGCCAGCCTATTCCCAAGGCGGCCCAACCCaCGGGCCGGTCTTGGGGTCAACCCCGGGTACC
149	SA1	184 CGCCAGCCTATTCCCAAGGCGGCCCAACCCaCGGGCCGGTCTTGGGGTCAACCCCGGGTACC
150	SA3	184 CGCCAGCCTATTCCCAAGGCGGCCCAACCCaCGGGCCGGTCTTGGGGTCAACCCCGGGTACC
151	SA13	184 CGtCAGCCTATcCCCAAGGCGGCCAGCCaCGGGCCGGTCTTGGGGTCAACCCCGGGTACC
146-153	consensus	CGcCAGCCTATtCCCAAGGCGGCCAaCCaCGGGcCGGTCTTGGGGTCAACCCCGGGTACC
153	SA11	245 CTTGGCCCTTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGcTGCTCTCCCCtCGAGG
152	SA6	245 CTTGGCCCTTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGTGTCTCTCCCCCGAGG
146	SA4	245 CTTGGCCCTTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGTGTCTCTCCCCCGAGG
147	SA5	245 CTTGGCCCTTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGTGTCTCTCCCCCGAGG
148	SA7	245 CTTGGCCCTTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGTGTCTCTCCCCCGAGG
149	SA1	245 CTTGGCCCTTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGTGTCTCTCCCCCGAGG
150	SA3	245 CTTGGCCCTTTTACGCCAATGAGGGCCTCGaTGGGCAGGGTGGTGTCTCTCCCCCGAGG
151	SA13	245 CTTGGCCCTTTATgCCCAATGAGGGCCTCGgTGGGCAGGGTGGTGTCTCTCCCCCGAGG
146-153	consensus	CTTGGCCCTTTTAcGCCAATGAGGGCCTCGgTGGGCAGGGTGGtTGCTCTCCCCcCGAGG
153	SA11	306 CTCTCGGCCTAACTGGGGCCCCCAATGA CCCCCCGCGCAAGATCGCGCAATTGGGGcAAGGTC
152	SA6	306 CTCTCGGCCTAAATTGGGGCCCCCAATGAC CCCCCCGCGCAAAATCGCGCAATTGGGTAAGGTC
146	SA4	306 CTCTCGGCCTAAATTGGGGCCCCCAATGAC CCCCCCGCGCAAAgTCGCGCAATTGGGTAAGGTC
147	SA5	306 CTCTCGGCCTAAATTGGGGCCCCCAATGAC CCCCCCGCGCAAAaTCGCGCAATTGGGTAAGGTC
148	SA7	306 CTCTCGGCCTAAATTGGGGCCCCCAATGA CCCCCCGCGCAAAgTCGCGCAATTGGGTAAGGTC
149	SA1	306 CTCTCGGCCTAAATTGGGGCCCCCAATGA CCCCCCGCGCAAAgTCGCGCAATTGGGTAAGGTC
150	SA3	306 CTCTCGGCCTAgTTGGGGCCCCCAAcGAC CCCCCCGCGCAAAATCGCGCAATTGGGTAAGGTC
151	SA13	306 CTCTCGGCCTAaTTGGGGCCCCCAATGAC CCCCCCGCGCAAAATCGCGCAAcTTGGGTAAGGTC
146-153	consensus	CTCTCGGCCTAaTTGGGGCCCCCAATGAC CCCCCCGCGCAaAaTCGCGCAATTTGGGTAAGGTC

FIGURE 6I-3

SEQ ID NO:	ISOLATE	
153	SA11	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
152	SA6	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
146	SA4	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
147	SA5	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
148	SA7	367 ATCGACACCCCTAACaTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
149	SA1	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
150	SA3	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
151	SA13	367 ATCGATACCCCTgACGTGCGGATTGCGCGAcCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
146-153	consensus	ATCGATACCCCTAACGTGCGGATTGCGCGAcCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
SEQ ID NO:	ISOLATE	
153	SA11	428 CCGTTGGGGCGTCGCAAGGGCCCTCGCACACGGTGTGAGAcTCTTGAGGACGGGGTAAAA
152	SA6	428 CCGTTGGGGCGTCGCAAGGGCCCTCGCACACGGTGTGAGGGTCTTGAGGACGGGGTAAAA
146	SA4	428 CCGTTGGGGCGTCGCAAGGGCCCTCGCACATGGTGTGAGGGTCTTGAGGACGGGGTAAAA
147	SA5	428 CCGTTGGGGCGTCGCAAGGGCCCTCGCACATGGTGTGAGGGTCTTGAGGACGGGGTAAAA
148	SA7	428 CCGTTGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGTCTTGAGGACGGGGTAAAA
149	SA1	428 CCGTTGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGTCTTGAGGACGGGGTAAAA
150	SA3	428 CCGTTGGGGCGTCGCAAGGGCTCTCGCACAcGGTGTGAGGGTCTTGAGGACGGGGTAAAA
151	SA13	428 CCGTTGGGGCGTCGCAAGGGCTCTCGCACAcGGTGTGAGGGTCTTGAGGACGGGGTAAAA
146-153	consensus	CCGTTGGGGCGTCGCAAGGGCTCTCGCACAcGGTGTGAGGGTCTTGAGGACGGGGTAAAA
SEQ ID NO:	ISOLATE	
153	SA11	489 tTATGCAACAGGGAATcTtCCCGTTGCTCTTTCTCcATCTTTaTCCTTGCACTTCTCTCG
152	SA6	489 CTATGCAACAGGGAATTGCCCCGGTTGCTCTTTCTCTATCTTTgTCCCTTGCACTTCTCTCG
146	SA4	489 CTATGCAACgGGGAATTGCCCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTCTCG
147	SA5	489 CTATGCAACAGGGAATTGCCCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTCTCG
148	SA7	489 tTACGCAACAGGGAATcTGCCCCGGTTGCTCTTTCTCTATCTTTaTCCTTGCACTTCTCTCG
149	SA1	489 CTACGCAACAGGGAATTGCCCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTCC
150	SA3	489 CTACGCAACAGGGAATTACCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTCA
151	SA13	489 CTATGCAACAGGGAATTACCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTCA
146-153	consensus	CTATGCAACaGGGAATtTgCCCCGGTTGCTCTTTCTCTAtCTTTTaTCCTTGCACTTCTCTCG

FIGURE 6I-4

<u>SEQ ID NO:</u>	<u>ISOLATE</u>
153	SA11
152	SA6
146	SA4
147	SA5
148	SA7
149	SA1
150	SA3
151	SA13
146-153	consensus

550	TGctTgACCGTCCCgGCCaCTGCA
550	TGcCTaACCGTCCCtGCCTCTGCA
550	TGcCTGACCGTCCCgGCCtCTGCA
550	TGctTGACCGTCCCAGCCTCTGCA
550	TGcCTGACCGTCCCAGCCTCcGCA
550	TGtCTGAtCaTCCCGGCCTCTGCA
550	TGcCTGACCGTCCCgGCCtCTGCA
550	TGcCTGACtGTCCCGaCCTCTGcC
	TGccTgAccgTCCCggCCtCtGCa

FIGURE 6J-1

SEQ ID NO:	Genotype	
103-154	cons.	
1	ATGAGCACgaaTCCTAAACCTCAAAGAAaAaACCaaAcGtAAcACcAaCCgcCGCCcAcagG	
103-124	1	ATGAGCACgAaTCCTAAACCTCAAAGAAaAaACCaaAcGTAACACCAaCCgcCGCCcACAGG
125-134	2	ATGAGCACAAaTCCTAAACCTCAAAGAAaAaACCaaAcGTAACACCAaCCgcCGCCcACAGG
135-138	3	ATGAGCACACTTCCTAAACCTCAAAGAAaAaACCaaAcGTAACACCAaCCgcCGCCcACAGG
139-145	4	ATGAGCACgAATCCTAAACCTCAAAGAAaAaACCaaAcGTAACACCAaCCgcCGCCcATGG
146-153	5	ATGAGCACGAATCCTAAACCTCAAAGAAaAaACCaaAcGTAACACCAaCCgcCGCCcACAGG
154	6	ATGAGCACACCTTCCAAaACCCCAAAGAAaAaACCaaAcGTAACACCAaCCgcCGCCcACAGG
SEQ ID NO:	Genotype	
103-154	cons.	
62	AcgTcaAGTTcCCgGGcGGtGGtCAGATCGTtGGtGGAGTtTactTgtTGCCCGCGCAGGGG	
103-124	1	ACGTCAAGTTCCCGGGcGGtGGtCAGATCGTtGGTGGAGTtTaccTgTTGCCCGCGCAGGGG
125-134	2	ACGTCAAGTTCCCGGGcGGcGGcCAGATCGTtGGCGGAGTtTactTgtTGCCCGCGCAGGGG
135-138	3	ACGTCAAGTTCCCGGGTGGCGGACAGATCGTtGGTGGAGTtTACGTgTTGCCCGCGCAGGGG
139-145	4	ACGTCAAGTTCCCGGGtGGtGGcCAGATCGTtGGCGGAGTtTactTgtTGCCCGCGCAGGGG
146-153	5	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTtGGTGGAGTtTactTgtTGCCCGCGCAGGGG
154	6	ACGTCAAGTTCCCGGGTGGCGGTcAGATCGTtGGCGGAGTtTactTgtTGCCCGCGCAGGGG
SEQ ID NO:	Genotype	
103-154	cons.	
123	CCCcaGgtTGGGTGTGCGCGcGgaCtaGgaAgaCTTCcGAGCGgTCgCAaCCtcGtGGaaGg	
103-124	1	CCCcaGgtTGGGTGTGCGCGCggaCtAGGAAGACTTCcGAGCGgTCgCAACCTCGtGGaaGg
125-134	2	CCCcAGgtTGGGTGTGCGCGCGACaAGGAAGaCTTCcGAGCGaTCCcAGCCcgCGTGGgAGg
135-138	3	CCCACGATtGGGTGTGCGCGCGACGCGTAaAACTTCGAAACGGTcaCAGCCTCGCGGACGa
139-145	4	CCCcaGgtTGGGTGTGCGCGcGgaCTcGgaAGACTTCGGAGCGGTcGCAACCTCGtGGcAGg
146-153	5	CCCtaGgtTGGGTGTGCGCGCGACTCGGAAGACTTCaGAACGGTCGCAACCCCGTGGgCGG
154	6	CCCCCGgtTGGGTGTGCGCGCGGACGAGAAAGACTTCcGAGCGGATCCcAGCCcAGAGGCAGG

FIGURE 6J-2

SEQ ID NO:	Genotype		
103-154	cons.		
184		CGaCAGCCTATcCCcAaAGGctCGcCggcccgagGGcaggtcCTGGGctcagCCcGGgtAcc	
103-124	1	CGaCAaCCTATCCCCAAGGctCGcCggCCCCGAGGGcAGGgCCTGGGctCAGCCcGGgtAcc	
125-134	2	CGCCAGCCCCATCCCGAAAGATCGGCGctCCACTGGCAAGtCCTGGGAaaCCaGGATATc	
135-138	3	CGACAGCCTATCCCCAAGGCGGTGGAGCGAAGGCCGgTCCTGGGCTCAGCCcGGGTACC	
139-145	4	CGtCAGCCTATCCCCAAGGCaCGtCggtccGAGGGcAGgTCCTGGGctCAGCCcGGGTACC	
146-153	5	CGcCAGCCTATtCCCCAAGGCGGCCAacCCaCGGGcCGGTCTCTGGGTCAACCCGGGTACC	
154	6	CGCCAACCTATATACCAAGGGCGCCAGCCCCAGGGCAGGCACtGGGCTCAGCCCCGATACC	
SEQ ID NO:	Genotype		
103-154	cons.		
245		CtTGGCCcctTcTATGgcaAtGAGGgcttcGgTGGGCaGgaTGGcTccTgTCCcCCcCgCGG	
103-124	1	CtTGGCCcCTCTATgCaAtGAGGGccttgGgTGGGCaGGATGGCTCCTGTCaCCCCgtGG	
125-134	2	CtTGGCCcCTgTATGGgAAtGAGGGcctCGGcTGGGCaGGtTGGCTCCTGTCCCCCGcGG	
135-138	3	CTTGGCCcCTCTATGTGTAAcGAGGGCTGCGGTGGGCaGGgTGGCTCCTGTCCCCACGCGG	
139-145	4	CtTGGCCcCTtTAcGGcAAtGAGGGcTGcGGGTGGGCaGGgTGGCTCcTGTcCCcCGcGG	
146-153	5	CTTGGCCcCTtTTAcGCCAAtGAGGGcCTCGgTGGGCaGGGTGGtTGTCTCCCCcCGAGG	
154	6	CTTGGCCcCTtTTATGGAAACGAGGGCTGTGGGTGGGCaGGtTGGCTCCTGTCCCCCGCGG	
SEQ ID NO:	Genotype		
103-153	cons.		
306		cTctcggCCtagtTGGGGcCccActGAcCCCCCGCGctaggTCgCGcAAttTGGgtAagGTC	
103-124	1	cTctCGGCCTAgT TGGGGCCCCaCaGACCCCCCGCGtAGGTGCGGTAAttTGGgtAAGGTC	
125-134	2	tTctCgtCCtctTGGGGCCCCActGAcCCCCGGCATAgATcGCGcAActTGGgtAagGTC	
135-138	3	CTCCGTCCATCTTGGGGCCCCAAcGACCCCCCGCGgaGGTCCCGCAATTTGGGTAAaGTC	
139-145	4	cTctcggCCgTCTTGGGGcCcaATGATCCCCCGCGAGgTCCCGcAAttTGGGTAAAGTC	
146-153	5	CTCTCGGCCTAatTGGGGCCCCAAcGACCCCCCGCGAaaTCGCGCAAtTTGGgtAAGGTC	
154	6	CTCCCGGCCACAT TGGGGCCCCCAATGACCCCCCGCGTCGATCCCGGAATTTGGGTAAAGTC	

FIGURE 6J-3

SEQ ID NO:	Genotype	
103-154	cons.	
367	ATCGATACCCtCACgTGcgGctTcGCCGAcCTCATGGGgTACaTcCCgcTCGTcGGcGccc	
367	ATCGATACCCtCaCaTGCGGCTTcGCCGACCTCATGGGTACATtCCGTCGTcGGcGccc	
367	ATCGATACCCtTaACgTGcgGctTtTGCCGACCTCATGGGgTACaTcCCcGTcGTtGGCGccc	
367	ATCGATACCCtTACGTGCGGAtTCGCCGACCTCATGGGTACATcCCCGTCGTcGGCGCTC	
367	ATCGATACcCTgACgTGcGGcTtTGCCGACCTCATGGGTACATcCCGTCGTaGGCGCCC	
367	ATCGATACCCtAACgTGCGGAtTCGCCGAcCTCATGGGTACATcCCCGTCGTAGCGGCC	
367	ATCGATACCCtAACGTGTGGGTTCGCCGATCTCATGGGTACATtCCCCGTCTGTGGCGCGC	
428	CcgTaGGgGGcGtcCGccaggGCCcTgGCGcATGGcGTcaGgggttcTgGAGACGGggtGAA	
428	CccTaGGgGGcGctTCCACAGGcCcTGGCGcATGGcGTCCGgGTtctTGGAGACGGCGTGAA	
428	CggTtGgaGGcGtGcCCAGAGctCTgGCaCATGGtGTgAGgTcCTGGAGGACGGgaTaaa	
428	CcGTAGgaGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGCCCCCTTGAAGACGGGATAAA	
428	CcGTgGgtGGCGTCGCCAGGcCcTgGCGcATGGcGTcAGGgtgTGGAGGACGGgaTCAA	
428	CCGTtGGGGCGTCGCAAGGGctCTcGCACaCGGTGTAGgGtctCTTgAGGACGGGGTAAA	
428	CTTtGGCGGGCGTCGCCGCTGCCCTCGCACATGGCGTGAGGGCAATCGAGGACGGGATCAA	
489	cTatGCAACaGGgAAttTgCCcGGTTGctCtTtTcTcTAtcTtTcTccTcTgGctcTgcTgTcc	
489	cTatGCAACAGGGAAtcTgCCcGGTTGctCtTtTcTcTATcTtTcTcTcTtTgGcttTgcTgTcc	
489	tTatGCAACaGGgAAttTgCCtGGTTGctCtTtTcTATcTtTcTcTcTtTgCctTtctGTcc	
489	TTTcGCAACAGGGAActTgCCCGGTTGCTCcTtTtTcTATcTtTcTcTcTtCTGTCTct	
489	cTatGCAACAGGGAAtCTTCCcGGTTGCTCtTtTcTcTATcTtTcTcTcTtTgGACtTctTCG	
489	cTatGCAACaGGgAAttTgCCCGGTTGCTCtTtTcTcTcTcTcTtTcTcTtTgCATTCTcTCg	
489	TTATGCAACAGGGAATCTCCCGGTTGCTCtTtTcTcTcTcTcTtTcTcTtTtTGGCACTACTCTCG	
SEQ ID NO:	Genotype	
103-154	cons.	
103-124	1	
125-134	2	
135-138	3	
139-145	4	
146-153	5	
154	6	
SEQ ID NO:	Genotype	
103-154	cons.	
103-124	1	
125-134	2	
135-138	3	
139-145	4	
146-153	5	
154	6	
SEQ ID NO:	Genotype	
103-154	cons.	
103-124	1	
125-134	2	
135-138	3	
139-145	4	
146-153	5	
154	6	

FIGURE 6J-4

<u>SEQ ID NO:</u>	<u>Genotype</u>	
103-154	cons.	550 TGcctgaccgtccCagcttCtgct
103-124	1	550 TGttTgACcatccCaGctTCcGct
125-134	2	550 TGCatCaCagtgcCaGtgTCtGct
135-138	3	550 TGctTAaTTcATCCaGCAGCTAGT
139-145	4	550 TGccTgACTgttCCagCgTCgGCC
146-153	5	550 TGccTgAccgTCCCGgCCtCtGCa
154	6	550 TGCCTCACAAAGCCAGCTTCGGCT

Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

SEQ ID NO:	Genotype	240	250	260	270	280	290	300	310	320	330	340
103-108	I/1a	tcagcccggtacccctgggcccctctatgcgaatgaggcttcgggtggcaggaatggctcctggtcctcgggctcctagttggggctccactgaccccgccgctagg										
109-124	I/1/b	TCAG-C-GT-C-T	CC-C-T-GCA-T	G-C-CTGG-GG	G-A	C-CC-G-t	C-GT-C	C-tGG-TAGC	C-CC-Ca-C			
125-128	II/1/b	TCAG-C-GT-C-T	CC-C-t-gGa-t	G-CaTG-Gg	A-A	C-CC-G-a	C-gc-c	C-tGG-TAGT	C-CC-Cg-C			
129-133	II/1/2a	AAAA-A-AT-C-C	cc-a-T-GGA-T	G-aCTC-GC	a-A	C-CC-G-C	G-A-T	C-cGT-TCTT	C-CC-ai-C			
134	IV/2b	AAGG-a-AT-T-T	CC-g-t-GAA-C	G-CTGG-Gc	A-T	C-CC-G-C	C-GC-G	T-cGT-TACT	C-CC-CT-C			
135-138	2c	AAGG-A-AT-C-T	CC-C-T-GGA-T	G-CCTC-GC	A-G	C-CC-G-C	C-GC-T	T-GGC-TTCA	C-CC-CC-C			
139	3a	TCAG-C-GT-C-T	CC-C-T-GTA-C	G-CTGG-GG	A-g	C-CC-G-C	A-GC-C	C-cGT-ATCT	C-CA-Ac-C			
140	4a	GCAG-C-GT-C-T	CC-C-T-GCA-T	G-CTGG-GG	A-G	C-CC-G-T	T-GC-C	C-tGG-ATCT	C-CA-AT-T			
141	4b	TCAG-C-GT-C-T	CC-T-C-GCA-T	G-CTGT-GG	A-G	C-CC-G-G	C-CC-C	C-tGG-GTCT	C-CC-AT-T			
142	4c	TCAG-C-GT-T-A	TC-T-C-GTA-T	G-TTGG-GG	9-A	C-CC-G-A	C-GT-C	T-CAGG-GTCT	C-CC-AT-T			
143	4d	TCAG-T-GT-T-T	TC-T-C-GCA-T	G-CTGG-GG	9-A	C-CC-G-A	C-GT-C	T-CGA-GTCT	t-CA-AT-T			
144	4e	TCAG-C-GT-C-T	TC-T-T-GTA-T	G-CTGT-GG	A-G	C-CC-G-A	C-GT-C	C-tGG-GTCT	C-CG-AT-T			
145	4f	TCAG-C-GT-C-T	TC-T-T-GTA-T	A-CTGT-GG	A-G	C-CC-G-C	C-GC-A	T-CGG-ATCT	C-AA-AT-T			
146	5a	TCAA-C-GT-C-T	CC-T-C-CCA-T	G-CCTC-GG	A-T	C-CC-G-C	C-GC-C	T-CGA-GTCT	C-CA-AT-T			
147	5b	TCAG-C-GT-C-T	CC-T-C-CCA-T	A-CTGT-GG	A-T	C-CC-G-C	C-GC-C	T-CGG-TAAT	C-CC-AT-T			
148	6a	TCAG-C-AT-C-T	TC-T-T-GAA-C	G-CTGT-GG	A-T	C-CC-G-C	C-GC-C	C-cGG-ACAT	C-CC-AT-C			

[illegible]

FIGURE 7A-1

SEQ ID NO:	ISOLATE	
156	US11	1 MSTNPKPQRTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
157	S14	1 MSTNPKPQRTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
158	SW1	1 MSTNPKPQRTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
159	S18	1 MSTNPKPQRTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
160	DR4	1 MSTNPKPQRTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
155	DK7	1 MSTNPKPQRTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
155-160	consensus	MSTNPKPQRTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
SEQ ID NO:	ISOLATE	
156	US11	62 RQIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
157	S14	62 RQIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
158	SW1	62 RQIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
159	S18	62 RQIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
160	DR4	62 RQIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
155	DK7	62 RQIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
155-160	consensus	RQIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
SEQ ID NO:	ISOLATE	
156	US11	123 IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEEDGVNYATGNLPGCSFSIFLLALLS
157	S14	123 IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEEDGVNYATGNLPGCSFSIFLLALLS
158	SW1	123 IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEEDGVNYATGNLPGCSFSIFLLALLS
159	S18	123 IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEEDGVNYATGNLPGCSFSIFLLALLS
160	DR4	123 IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEEDGVNYATGNLPGCSFSIFLLALLS
155	DK7	123 IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEEDGVNYATGNLPGCSFSIFLLALLS
155-160	consensus	IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEEDGVNYATGNLPGCSFSIFLLALLS

FIGURE 7A-2

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
156	US11	184 CLTVPASA
157	S14	184 CLTVPASA
158	SW1	184 CLTVPASA
159	S18	184 CLTVPASA
160	DR4	184 CLTVPASA
155	DK7	184 CLTVPASA
155-160	consensus	CLTVPASA

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REPLACEMENT SHEET

SEQ ID NO: ISOLATE

161-176 consensus

SEO ID NO: ISOLATE

161-176 consensus

RQIPKARrPEGRaWAQPGyPWPLYgnEG-GWAGWLLSPrGSRPpSWGpTDPRRRSrNLGKV

FIGURE 7B-2

SEQ ID NO:	ISOLATE	
175	P8	123 IDTLTCGFADLMGYIPLVGgPLGGvARALAHGVRVvEDGVNYATGNLPGCSFSIFLLALLS
170	IND8	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
162	S45	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
171	S9	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
163	D1	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
165	P10	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
169	IND3	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
164	US6	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
166	DK1	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
167	T10	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
168	SW2	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
161	SA10	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
174	HK4	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
172	HK3	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
176	T3	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
173	HK5	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
161-176	consensus	IDTLTCGFADLMGYIPLVGaPLGGaARALAHGVRVLEdGVNYATGNLPGCsFSIFLLALLS
SEQ ID NO:	ISOLATE	
175	P8	184 CLTiPaSA
170	IND8	184 CLTiVPaSA
162	S45	184 CLTiPaSA
171	S9	184 CLTiPaSA
163	D1	184 CLTiPaSA
165	P10	184 CLTiPaSA
169	IND3	184 CLTiPaSA
164	US6	184 CLTiPaSA
166	DK1	184 CLTiPaSA
167	T10	184 CLTiPaSA
168	SW2	184 CLTiPaSA
161	SA10	184 CLTiPaSA
174	HK4	184 CLTiPaSA
172	HK3	184 CLTiPaSA
176	T3	184 CLTiPaSA
173	HK5	184 CLTiPvSA
161-176	consensus	CLTiPaSA

FIGURE 7C-1

SEQ ID NO:	ISOLATE	
173	HK5	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
176	T3	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
172	HK3	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
174	HK4	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
161	SA10	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
168	SW2	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
167	T10	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
166	DK1	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
164	US6	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
169	IND3	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
165	P10	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
163	D1	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
156	US11	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
157	S14	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
158	SW1	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
159	S18	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
160	DR4	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
155	DK7	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
170	IND8	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
162	S45	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
171	S9	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
175	P8	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR
155-176	consensus	MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGPRPRLGVRATRKTSESSQPRGR

FIGURE 7C-2

SEQ ID NO:	ISOLATE	
173	HK5	62 RQIPKARRPEGRtWAQPGYPWPPLYGnEGMGWAGWLLSPhGSRPsWGPTDPRRRSRNLGKV
176	T3	62 RQIPKARRPEGRaWAQPGYPWPPLYGdEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
172	HK3	62 RQIPKARQEGRTWAQPGYPWPPLYGNEGMGAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
174	HK4	62 RQIPKARQEGRTWAQPGYPWPPLYGNEGMGAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
161	SA10	62 RQIPKARQEGRTWAQPGYPWPPLYGNEGLGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
168	SW2	62 RQIPKARQEGRTWAQPGYPWPPLYGNEGMGAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
167	T10	62 RQIPKARQEGRTWAQPGYPWPPLYGNEGMGAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
166	DK1	62 RQIPKARRPEGRaWAQPGYPWPPLYGNEGMGAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
164	US6	62 RQIPKARRPEGRaWAQPGYPWPPLYGNEGMGAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
169	IND3	62 RQIPKARRPEGRaWAQPGYPWPPLYGNEGLGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
165	P10	62 RQIPKARRPEGRaWAQPGYPWPPLYGNEGLGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
163	D1	62 RQIPKARRPEGRaWAQPGYPWPPLYGNEGLGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
156	US11	62 RQIPKARRPEGRtWAQPGYPWPPLYGNEGCCGAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
157	S14	62 RQIPKARRPEGRtWAQPGYPWPPLYGNEGCCGAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
158	SW1	62 RQIPKARRPEGRtWAQPGYPWPPLYGNEGCCGAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
159	S18	62 RQIPKARRPEGRtWAQPGYPWPPLYGNEGCCGAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
160	DR4	62 RQIPKARRPEGRtWAQPGYPWPPLYGNEGCCGAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
155	DK7	62 RQIPKARRPEGRtWAQPGYPWPPLYGNEGCCGAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
170	IND8	62 RQIPKARRPEGRaWAQPGHPWPPLYGNEGLGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
162	S45	62 RQIPKARRPEGRaWAQPGHPWPPLYGNEGLGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
171	S9	62 RQIPKARhPEGRaWAQPGYPWPPLYGNEGLGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
175	P8	62 RQIPKARrPEGRaWAQPGhWPPLYaNEGLGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
155-176	consensus	RQIPKARrPEGRaWAQPGYPWPPLYgnEG-GWAGWLLSPRGSRPsWGPTDPRRRSRNLGKV

FIGURE 7C-3

SEQ ID NO:	ISOLATE	
173	HK5	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
176	T3	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
172	HK3	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
174	HK4	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
161	SA10	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
168	SW2	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
167	T10	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
166	DK1	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
164	US6	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
169	IND3	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
165	P10	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
163	D1	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
156	US11	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
157	S14	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
158	SW1	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
159	S18	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
160	DR4	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
155	DK7	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
170	IND8	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
162	S45	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
171	S9	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
175	P8	123 IDTLTCGFADLMGYIPLVGgPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
155-176	consensus	IDTLTCGFADLMGYIPLVGaPLGGaARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

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Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

FIGURE 7C-4

SEQ ID NO:	ISOLATE	
173	HK5	184 CLTtPvSA
176	T3	184 CLTiPaSA
172	HK3	184 CLTtPaSA
174	HK4	184 CLTiPaSA
161	SA10	184 CLTtPaSA
168	SW2	184 CLTiPaSA
167	T10	184 CLTtPaSA
166	DK1	184 CLTiPaSA
164	US6	184 CLTtPaSA
169	IND3	184 CLTiPaSA
165	P10	184 CLTtPaSA
163	D1	184 CLTiPaSA
156	US11	184 CLTVPASA
157	S14	184 CLTVPASA
158	SW1	184 CLTVPASA
159	S18	184 CLTVPASA
160	DR4	184 CLTVPASA
155	DK7	184 CLTVPASA
170	IND8	184 CLTVPASA
162	S45	184 CLTiPaSA
171	S9	184 CLTtPaSA
175	P8	184 CLTiPaSA
155-176	consensus	CLTiPaSA

FIGURE 7D

SEQ ID NO:	ISOLATE	
179	T9	1 MSTNPKPQRKT:RNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRTTRKTSERSQPRGR
178	US10	1 MSTNPKPQRKT:RNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
180	T2	1 MSTiPKPQRKT:RNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
177	T4	1 MSTnPKPQRKT:RNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
177-180	consensus	MSTnPKPQRKT:RNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRaTRKTSERSQPRGR
SEQ ID NO:	ISOLATE	
179	T9	62 RQIPKDRRsTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPpDPRHRSRNVGKV
178	US10	62 RQIPKDRRsTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPtDPRHRSRNVGKV
180	T2	62 RQIPKDRRsTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNVGKV
177	T4	62 RQIPKDRRsTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNVGKV
177-180	consensus	RQIPKDRRsTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPnDPRHRSRNVGKV
SEQ ID NO:	ISOLATE	
179	T9	123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
178	US10	123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
180	T2	123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
177	T4	123 IDTLTCsIADLMGYvPVVGgPLGGVARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
177-180	consensus	IDTLTCgfADLMGYiPVVGaPLGGVARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
SEQ ID NO:	ISOLATE	
179	T9	184 CITtPaSA
178	US10	184 CITiPvSA
180	T2	184 CITiPvSA
177	T4	184 CITiPvSA
177-180	consensus	CITiPvSA

FIGURE 7E

SEQ ID NO:	ISOLATE	
183	DK11	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRtTRKTSERSQPRGR
184	SW3	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
181	T8	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
182	US1	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
185	DK8	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
181-185	consensus	MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRaTRKtSERSQPRGR
SEQ ID NO:	ISOLATE	
183	DK11	62 RQIPKDRRSTGKpWGKPGYPWPPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHkSRNLGKV
184	SW3	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHrSRNLGKV
181	T8	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGrV
182	US1	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGKV
185	DK8	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGKV
181-185	consensus	RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGsRpTtWGPTDPRHrSRNLGKV
SEQ ID NO:	ISOLATE	
183	DK11	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEdGINyATGNLPGCSFSIFLLALLS
184	SW3	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEdGINyATGNLPGCSFSIFLLALLS
181	T8	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEdGINyATGNLPGCSFSIFLLALLS
182	US1	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEdGINyATGNLPGCSFSIFLLALLS
185	DK8	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEdGINyATGNLPGCSFSIFLLALLS
181-185	consensus	IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEdGINyATGNLPGCSFSIFLLALLS
SEQ ID NO:	ISOLATE	
183	DK11	184 CcTVPVSA
184	SW3	184 CFTVPVSA
181	T8	184 CFTVPVSA
182	US1	184 CaTVPVSA
185	DK8	184 CcTVPVSA
181-185	consensus	C-TVPVSA

FIGURE 7F-1

SEQ ID NO:	ISOLATE	
183	DK11	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRtTRKTSERSQPRGR
184	SW3	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
181	T8	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
182	US1	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
185	DK8	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
186	S83	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
178	US10	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
180	T2	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
179	T9	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRtTRKTSERSQPRGR
177	T4	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRaTRKTSERSQPRGR
177-186	consensus	MSTnPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRaTRKtSERSQPRGR
183	DK11	62 RQIPKDRRSTGKpWGKPGYPWPPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHkSRNLGKV
184	SW3	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHRSRNLGKV
181	T8	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGrV
182	US1	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV
185	DK8	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV
186	S83	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV
178	US10	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHkSRNLGKV
180	T2	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV
179	T9	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV
177	T4	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV
177-186	consensus	RQIPKDRRSTGKsWGKPGYPWPPLYGNEG-GWAGWLLSPRGStPwWGPTDPRHrSRNLGKV

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Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

FIGURE 7F-2

SEQ ID NO:	ISOLATE	
183	DK11	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNTLPGCSFSIFLLALLS
184	SW3	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNTLPGCSFSIFLLALLS
181	T8	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNTLPGCSFSIFLLALLS
182	US1	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNTLPGCSFSIFLLALLS
185	DK8	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNTLPGCSFSIFLLALLS
186	S83	123 IDTLTCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNTLPGCSFSIFLLALLS
178	US10	123 IDTLTCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNTLPGCSFSIFLLALLS
180	T2	123 IDTLTCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNTLPGCSFSIFLLALLS
179	T9	123 IDTLTCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNTLPGCSFSIFLLALLS
177	T4	123 IDTLTCSLADLMGYVPVVGgPLGGVARALAHGVRVLEDDGINYATGNTLPGCSFSIFLLALLS
177-186	consensus	IDT-TCGfADLMGYiPVVGaPvGGVARALAHGVRVLEDDGiNYATGNTLPGCSFSIFLLALLS
SEQ ID NO:	ISOLATE	
183	DK11	184 CcTVPVSA
184	SW3	184 CFTVPVSA
181	T8	184 CFTVPVSA
182	US1	184 CaTVPVSA
185	DK8	184 CcTVPVSA
186	S83	184 CIsVPVSA
178	US10	184 CITIPVSA
180	T2	184 CITIPVSA
179	T9	184 CITtPaSA
177	T4	184 CITiPvSA
177-186	consensus	CitvPvSA

FIGURE 7G

SEQ ID NO:	ISOLATE	
189	S2	1 MSTLPKPQPKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATKTSERSQPRGR
187	HK10	1 MSTLPKPQPKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATKTSERSQPRGR
190	DK12	1 MSTLPKPQPKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATKTSERSQPRGR
188	S52	1 MSTLPKPQPKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATKTSERSQPRGR
187-190	consensus	MSTLPKPQPKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATKTSERSQPRGR
SEQ ID NO:	ISOLATE	
189	S2	62 RQIPKARRSEGRSWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
187	HK10	62 RQIPKARRSEGRSWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
190	DK12	62 RQIPKARRSEGRSWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
188	S52	62 RQIPKARRSEGRSWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
187-190	consensus	RQIPKARRSEGRSWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
SEQ ID NO:	ISOLATE	
189	S2	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
187	HK10	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
190	DK12	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
188	S52	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
187-190	consensus	IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
SEQ ID NO:	ISOLATE	
189	S2	184 CLIHPAAS
187	HK10	184 CLIHPAAS
190	DK12	184 CLIHPAAS
188	S52	184 CLVHPAAS
187-190	consensus	CLIHPAAS

FIGURE 7H-1

SEQ ID NO:	ISOLATE
194	Z5
193	Z1
192	Z8
195	Z6
196	Z7
191	Z4
197	DK13
191-197	consensus

1	MSTNPKPQRTKRTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRatRKTSESRQPRGR
1	MSTNPKPQRTKRTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRaARKTSESRQPRGR
1	MSTNPKPQRTKRTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1	MSTNPKPQRTKRTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1	MSTNPKPQRTKRTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRtTRKTSESRQPRGR
1	MSTNPKPQRTKRTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1	MSTNPKPQRTKRTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1	MSTNPKPQRTKRTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRatRKTSESRQPRGR
191-197	consensus

SEQ ID NO:	ISOLATE
194	Z5
193	Z1
192	Z8
195	Z6
196	Z7
191	Z4
197	DK13
191-197	consensus

62	RQIPqARRSEGRSWAQPgyPWPPLYGNEGCGWAGWLLSPRGSRPSWGqNDPRRRSRNLGKV
62	RQIPkARRSEGRSWAQPgyPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV
62	RQIPkARRSEGRSWAQPgyPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV
62	RQIPkARRSEGRSWAQPgyPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV
62	RQIPkARRSEGRSWAQPgyPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV
62	RQIPkARQSEGRSWAQPgyPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV
62	RQIPkARQIEGRSWAQPgyPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV
191-197	consensus

FIGURE 7H-2

SEQ ID NO:	ISOLATE	
194	Z5	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAL EDGINYATGNLPGCSFSIFLLALfs
193	Z1	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS
192	Z8	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS
195	Z6	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS
196	Z7	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAL EDGINYATGNLPGCSFSIFLLALLS
191	Z4	123 IDTLTCGFADLMGYIPIVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS
197	DK13	123 IDTLTCGFADLMGYIPVVGAPVGGVARALAHGVR11 EDGVNYATGNLPGCSFSIFLLALLS
191-197	consensus	IDTLTCGFADLMGYIPIVGAPVGGVARALAHGVRavedGiNYATGNLPGCSFSIFLLALLS
184	CLTTPASA	184 CLTTPASA
184	CLTTPASA	184 CLTTPASA
184	CLTVPtSA	184 CLTVPtSA
184	CLTVPASA	184 CLTVPASA
184	CLTVPASA	184 CLTVPASA
184	CLTVPASA	184 CLTVPASA
191-197	consensus	CLTVPaSa

[illegible]

FIGURE 71-2

SEQ ID NO:	ISOLATE	
205	SA11	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRaLEDGVNYATGNLPGCCSFSIFILALLS
202	SA3	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCCSFSIFILALLS
198	SA4	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCCSFSIFILALLS
199	SA5	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCCSFSIFILALLS
200	SA7	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCCSFSIFILALLS
203	SA13	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCCSFSIFILALLS
201	SA1	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCCSFSIFILALLS
204	SA6	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCCSFSIFVLLLS
198-205	consensus	IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCCSFSIFILALLS
205	ISOLATE	184 CLTVPaTa
202	SA3	184 CLTVPaSA
198	SA4	184 CLTVPaSA
199	SA5	184 CLTVPaSA
200	SA7	184 CLTVPaSA
203	SA13	184 CLTVPtSA
201	SA1	184 CLiPaSA
204	SA6	184 CLtvPaSA
198-205	consensus	CLtvPaSA

FIGURE 7J

SEQ ID NO:	Genotype	
155-206	cons.	1 MSThPKPQRKTKRNTnRRPQDVKFPGGGQIVGGVILLPRRGPRLGVRaTKtSERSQPRGRROIPKaRtpeGrSwagQpGYPWPLYgnEGGcgWAGW
155-176	type 1	MSThPKPQRKTKRNTnRRPQDVKFPGGGQIVGGVILLPRRGPRLGVRaTKtSERSQPRGRROIPKaRtpeGrSwagQpGYPWPLYgnEGGcgWAGW
177-186	type 2	MSThPKPQRKTKRNTnRRPQDVKFPGGGQIVGGVILLPRRGPRLGVRaTKtSERSQPRGRROIPKaRtpeGrSwagQpGYPWPLYgnEGGcgWAGW
187-190	type 3	MSThPKPQRKTKRNTnRRPQDVKFPGGGQIVGGVILLPRRGPRLGVRaTKtSERSQPRGRROIPKaRtpeGrSwagQpGYPWPLYgnEGGcgWAGW
191-197	type 4	MSThPKPQRKTKRNTnRRPQDVKFPGGGQIVGGVILLPRRGPRLGVRaTKtSERSQPRGRROIPKaRtpeGrSwagQpGYPWPLYgnEGGcgWAGW
198-205	type 5	MSThPKPQRKTKRNTnRRPQDVKFPGGGQIVGGVILLPRRGPRLGVRaTKtSERSQPRGRROIPKaRtpeGrSwagQpGYPWPLYgnEGGcgWAGW
206	type 6	MSThPKPQRKTKRNTnRRPQDVKFPGGGQIVGGVILLPRRGPRLGVRaTKtSERSQPRGRROIPKaRtpeGrSwagQpGYPWPLYgnEGGcgWAGW
155-206	cons.	97 LLSPrGSRpSwGpDPRrSRNIGKVIDTITCGfADLMGYIPLVGaPIGGVaRALAHGVRVLEDGVNvATeNLPCCsFSIFILLALLSCLtYPaSa
155-176	type 1	LLSPrGSRpSwGpDPRrSRNIGKVIDTITCGfADLMGYIPLVGaPIGGVaRALAHGVRVLEDGVNvATeNLPCCsFSIFILLALLSCLtYPaSa
177-186	type 2	LLSPrGSRpSwGpDPRrSRNIGKVIDTITCGfADLMGYIPLVGaPIGGVaRALAHGVRVLEDGVNvATeNLPCCsFSIFILLALLSCLtYPaSa
187-190	type 3	LLSPrGSRpSwGpDPRrSRNIGKVIDTITCGfADLMGYIPLVGaPIGGVaRALAHGVRVLEDGVNvATeNLPCCsFSIFILLALLSCLtYPaSa
191-197	type 4	LLSPrGSRpSwGpDPRrSRNIGKVIDTITCGfADLMGYIPLVGaPIGGVaRALAHGVRVLEDGVNvATeNLPCCsFSIFILLALLSCLtYPaSa
198-205	type 5	LLSPrGSRpSwGpDPRrSRNIGKVIDTITCGfADLMGYIPLVGaPIGGVaRALAHGVRVLEDGVNvATeNLPCCsFSIFILLALLSCLtYPaSa
206	type 6	LLSPrGSRpSwGpDPRrSRNIGKVIDTITCGfADLMGYIPLVGaPIGGVaRALAHGVRVLEDGVNvATeNLPCCsFSIFILLALLSCLtYPaSa